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McGarry
09/490208
Seq. ID 3 w/ Interf

GenCore version 5.1.4_p5_4578

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Run on: March 14, 2003, 08:46:58 ; Search time 8468 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	167	71	1.7	512	63	US-60-198-833-4 Sequence 4, Appli

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c 169	69	1.7	301	62	US-60-181-428-71	Sequence 71, Appl
c 170	69	1.7	301	62	US-60-181-428-72	Sequence 72, Appl
171	66	1.6	661	61	US-60-177-571-1027	Sequence 1027, Ap
172	66	1.6	663	64	US-60-205-203-2	Sequence 2, Appli
173	64	1.5	379	60	US-60-163-233-757	Sequence 757, App
174	64	1.5	379	63	US-60-198-833-9	Sequence 9, Appli
175	64	1.5	563	61	US-60-173-469-365	Sequence 365, App
176	64	1.5	634	63	US-60-196-190-315	Sequence 315, App
177	64	1.5	1519	66	US-60-229-514-107	Sequence 107, App
c 178	63	1.5	451	60	US-60-162-247-1700	Sequence 1700, Ap
c 179	63	1.5	451	60	US-60-169-840-3060	Sequence 3060, Ap
180	62	1.5	215	30	US-09-760-475-1616	Sequence 1616, Ap
c 181	62	1.5	618	60	US-60-162-247-2440	Sequence 2440, Ap
c 182	62	1.5	619	60	US-60-163-233-565	Sequence 565, App
183	62	1.5	641	60	US-60-162-247-2096	Sequence 2096, Ap
184	62	1.5	642	60	US-60-163-233-1152	Sequence 1152, Ap
c 185	62	1.5	699	61	US-60-177-571-1897	Sequence 1897, Ap
c 186	62	1.5	699	61	US-60-177-646-1517	Sequence 1517, Ap
187	62	1.5	704	62	US-60-188-162-123	Sequence 123, App
188	62	1.5	704	62	US-60-188-162-981	Sequence 981, App
189	62	1.5	704	64	US-60-205-224-2	Sequence 2, Appli
c 190	62	1.5	784	24	US-09-634-306B-112871	Sequence 112871,
c 191	62	1.5	784	38	US-10-027-632-112871	Sequence 112871,
c 192	62	1.5	2191	62	US-60-185-361-212	Sequence 212, App
c 193	62	1.5	2191	62	US-60-185-361-213	Sequence 213, App
194	60	1.4	60	34	US-09-908-975-32057	Sequence 32057, A
195	60	1.4	60	34	US-09-908-975-32228	Sequence 32228, A
196	60	1.4	60	34	US-09-908-975A-32057	Sequence 32057, A
197	60	1.4	60	34	US-09-908-975A-32228	Sequence 32228, A
198	60	1.4	60	72	US-60-287-724-32057	Sequence 32057, A
199	60	1.4	60	72	US-60-287-724-32228	Sequence 32228, A
200	60	1.4	254	6	US-08-293-347-1820	Sequence 1820, Ap
201	60	1.4	254	20	US-09-534-845-6000	Sequence 6000, Ap
202	60	1.4	254	20	US-09-534-846-6000	Sequence 6000, Ap
203	58	1.4	401	60	US-60-162-247-2701	Sequence 2701, Ap
204	58	1.4	402	60	US-60-162-247-698	Sequence 698, App
205	58	1.4	402	60	US-60-163-233-950	Sequence 950, App
206	58	1.4	402	60	US-60-169-840-2514	Sequence 2514, Ap
207	58	1.4	402	60	US-60-169-867-2303	Sequence 2303, Ap
208	56	1.4	1284	62	US-60-185-361-433	Sequence 433, App
209	56	1.4	1727	62	US-60-185-361-101	Sequence 101, App
210	54	1.3	684	64	US-60-207-189-4	Sequence 4, Appli
211	53	1.3	515	61	US-60-171-481-5	Sequence 5, Appli
212	53	1.3	515	61	US-60-171-481-658	Sequence 658, App
213	52	1.3	60	34	US-09-908-975-8469	Sequence 8469, Ap
214	52	1.3	60	34	US-09-908-975A-8469	Sequence 8469, Ap
215	52	1.3	60	72	US-60-287-724-8469	Sequence 8469, Ap
216	51	1.2	51	61	US-60-172-373-1020	Sequence 1020, Ap
217	51	1.2	51	76	US-60-324-185-13873	Sequence 13873, A
218	51	1.2	549	63	US-60-196-190-284	Sequence 284, App
c 219	50	1.2	304	63	US-60-198-833-1	Sequence 1, Appli
c 220	50	1.2	552	61	US-60-171-481-28	Sequence 28, Appl
221	50	1.2	841	26	US-09-667-117-117	Sequence 117, App
222	50	1.2	841	26	US-09-667-117A-117	Sequence 117, App
223	50	1.2	841	60	US-60-167-542-208	Sequence 208, App
224	50	1.2	855	61	US-60-172-373-14898	Sequence 14898, A

ALIGNMENTS

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RESULT 1
PCT-US01-01381A-3
; Sequence 3, Application PC/TUS0101381A
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTSP-0098
;  CURRENT APPLICATION NUMBER: PCT/US01/01381A
;  CURRENT FILING DATE:  2001-01-16
;  PRIOR APPLICATION NUMBER: 09/490,208
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 3
;   LENGTH: 4145
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (207)...(3668)
PCT-US01-01381A-3

  Query Match            100.0%;  Score 4145;  DB 1;  Length 4145;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
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Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
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Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
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Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

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Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
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RESULT 2
PCT-US01-01381A-10
; Sequence 10, Application PC/TUS0101381A
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0098
; CURRENT APPLICATION NUMBER: PCT/US01/01381A
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 10
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)...(4110)
PCT-US01-01381A-10

Query Match 100.0%; Score 4145; DB 1; Length 4145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
```

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Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
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Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
```

RESULT 3
US-08-630-798-1
; Sequence 1, Application US/08630798
; GENERAL INFORMATION:
; APPLICANT: Timothy R. Billiar
; APPLICANT: Edith Tzeng
; APPLICANT: Andreas K. Nussler
; APPLICANT: David A. Geller
; APPLICANT: Richard K. Simmons
; APPLICANT: Larry L. Shears II
; TITLE OF INVENTION: Inducible Nitric Oxide Synthase
; TITLE OF INVENTION: Gene for Treatment of Disease
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market Street, Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,798
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Lewis F. Jr.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 119130-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6020
; TELEFAX: (215) 575-6015
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
; DESCRIPTION: Synthase cDNA Clone
; HYPOTHETICAL: NO

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;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       TISSUE TYPE:  Induced Human Hepatocyte RNA
;     IMMEDIATE SOURCE:
;       LIBRARY:  Lambda Zap II cDNA
;       CLONE:  pHINOS
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:  unknown
;       MAP POSITION:  unknown
;       UNITS:  unknown
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  207..3668
;       IDENTIFICATION METHOD:  Experiment
US-08-630-798-1

  Query Match             100.0%;  Score 4145;  DB 10;  Length 4145;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy    1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy    1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy    1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy    1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
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Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
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Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
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Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
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Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
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Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
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Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
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Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
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Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
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RESULT 4
US-09-053-375B-110
; Sequence 110, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvilli, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-110

Query Match 100.0%; Score 4145; DB 14; Length 4145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
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Db      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
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Db    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
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Db    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
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Db    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

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Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

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Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
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Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
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Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

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Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

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Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
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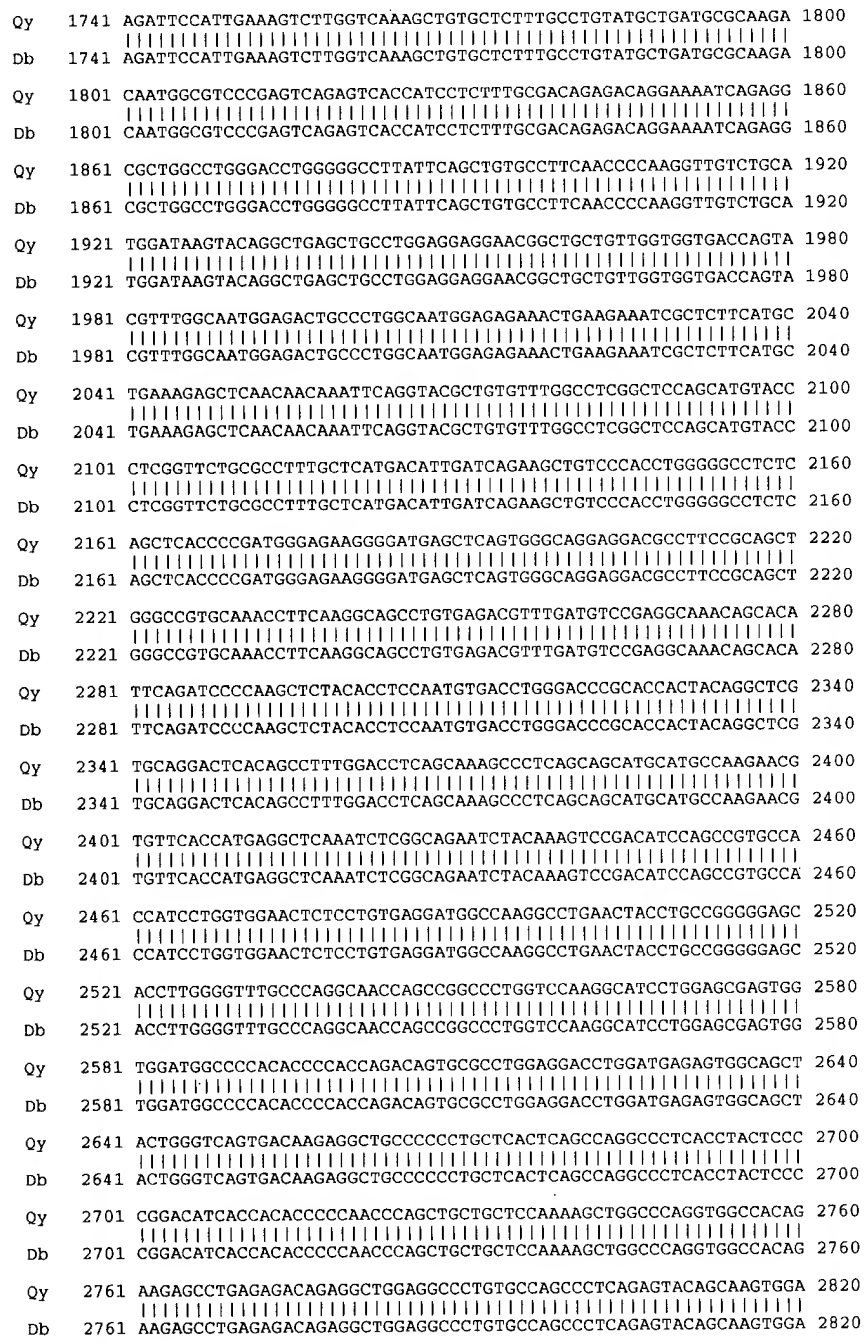
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Db 2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
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RESULT 5
US-09-176-496-1
; Sequence 1, Application US/09176496A
; GENERAL INFORMATION:
; APPLICANT: Billiar, Timothy R.
; APPLICANT: Tzeng, Edith
; APPLICANT: Nussler, Andreas K.
; APPLICANT: Geller, David A.
; APPLICANT: Simmons, Richard K.
; APPLICANT: Shears II, Larry L.
; TITLE OF INVENTION: Inducible Nitric Oxide Synthase Gene for Treatment of
; TITLE OF INVENTION: Disease
; FILE REFERENCE: 187868
; CURRENT APPLICATION NUMBER: US/09/176,496A
; CURRENT FILING DATE: 1998-10-21
; EARLIER APPLICATION NUMBER: 08/465,522
; EARLIER FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: 08/314,917
; EARLIER FILING DATE: 1994-09-28
; EARLIER APPLICATION NUMBER: 07/981,344
; EARLIER FILING DATE: 1992-11-25
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Induced Human Hepatocyte RNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (207)..(3668)
US-09-176-496-1

Query Match 100.0%; Score 4145; DB 15; Length 4145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
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Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Qy  1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Db  1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Qy  1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Db  1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Qy  1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Db  1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Qy  1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Db  1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Qy  1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Db  1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Qy  1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Db  1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Qy  1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Db  1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Qy  1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Db  1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Qy  1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Db  1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Qy  1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Db  1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Qy  1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Db  1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Qy  2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Db  2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Qy  2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Db  2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Qy  2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Db  2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Qy  2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Db  2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Qy  2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Db  2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Qy  2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Db  2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Qy  2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Db  2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
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Qy  2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Db  2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Qy  2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Db  2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Qy  2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Db  2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Qy  2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Db  2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Qy  2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Db  2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Qy  2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Db  2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Qy  2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Db  2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Qy  2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Db  2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Qy  2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Db  2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Qy  3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Db  3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Qy  3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Db  3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Qy  3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Db  3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Qy  3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Db  3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Qy  3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
Db  3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
Qy  3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
Db  3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
Qy  3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
Db  3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
Qy  3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
Db  3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
Qy  3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
Db  3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
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Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
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RESULT 6
US-09-440-302A-724
; Sequence 724, Application US/09440302A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 724
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-440-302A-724

Query Match 100.0%; Score 4145; DB 18; Length 4145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
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Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
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Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
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Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
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Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
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Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
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Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
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Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
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Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
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Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
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Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGACGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
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RESULT 7
US-09-440-302B-724
; Sequence 724, Application US/09440302B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 724
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-440-302B-724

Query Match 100.0%; Score 4145; DB 18; Length 4145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
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Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
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Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
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Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
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Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
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Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
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Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
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Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
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Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
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Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
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Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
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Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
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Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
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Db    3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy    3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy    3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy    3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy    3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy    3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy    3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy    3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy    3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy    3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy    3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy    3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy    3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy    3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy    3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy    4141 TAATC 4145
           |||||
Db    4141 TAATC 4145

RESULT 8
US-09-442-589B-758
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; Sequence 758, Application US/09442589B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey
;  TITLE OF INVENTION: Human Cardiovascular Array
;  FILE REFERENCE: CLON-006CIP10
;  CURRENT APPLICATION NUMBER: US/09/442,589B
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 1194
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 758
;   LENGTH: 4145
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-442-589B-758

  Query Match             100.0%;  Score 4145;  DB 18;  Length 4145;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
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Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
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Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
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Db    2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy    3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Db    3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy    3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Db    3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy    3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Db    3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy    3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Db    3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy    3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
Db    3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy    3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
Db    3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy    3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
Db    3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy    3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
Db    3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy    3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
Db    3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy    3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
Db    3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy    3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
Db    3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy    3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
Db    3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy    3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
Db    3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy    3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
Db    3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy    3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
Db    3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy    3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
Db    3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy    3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
Db    3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
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Db    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
Db    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy    4141 TAATC 4145
Db    4141 TAATC 4145
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RESULT 9
US-09-490-208-3
; Sequence 3, Application US/09490208A
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE E
; FILE REFERENCE: RTS-0066
; CURRENT APPLICATION NUMBER: US/09/490,208A
; CURRENT FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 3
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (207)...(3668)
US-09-490-208-3

Query Match 100.0%; Score 4145; DB 18; Length 4145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
Db     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
Db     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
Db     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
Db     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
Db     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
Db     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
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Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
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Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
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Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
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Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
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RESULT 10
US-09-490-208-10
; Sequence 10, Application US/09490208A
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE E
; FILE REFERENCE: RTS-0066
; CURRENT APPLICATION NUMBER: US/09/490,208A
; CURRENT FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 10
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)...(4110)
US-09-490-208-10

Query Match 100.0%; Score 4145; DB 18; Length 4145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
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Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
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Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
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Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
Qy   4141 TAATC 4145
Db   4141 TAATC 4145
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RESULT 11
US-09-543-679A-2507
; Sequence 2507, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICTION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:

```
;            TELEPHONE: 609-409-3035
;            TELEFAX: 413-254-9245
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2507:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 4145 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2507:
US-09-543-679A-2507

  Query Match            100.0%;  Score 4145;  DB 21;  Length 4145;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
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Db     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
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Db     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy    1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy    1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy    1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy    1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy    1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy  1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy  2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy  2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy  2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy  2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy  2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy  2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy  2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy  2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy  2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy  2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy  2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy  2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy  2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy  2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy  2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy  2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy  3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy  3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy  3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy  3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy  3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy  3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy  3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy  3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy  3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy  3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy  3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy  3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy  3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy  3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy  3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy  3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy  3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy  4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy  4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
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Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145


RESULT 12
US-10-182-049-3
; Sequence 3, Application US/10182049
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSIO
;  FILE REFERENCE: RTSP-0360
;  CURRENT APPLICATION NUMBER: US/10/182,049
;  CURRENT FILING DATE:  2002-07-27
;  PRIOR APPLICATION NUMBER: 09/490,208
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 3
;   LENGTH: 4145
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (207)...(3668)
US-10-182-049-3

  Query Match             100.0%;  Score 4145;  DB 41;  Length 4145;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
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Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
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Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
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Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
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Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
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Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
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RESULT 13
US-10-182-049-10
; Sequence 10, Application US/10182049
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSIC
; FILE REFERENCE: RTSP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 10
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)...(4110)
US-10-182-049-10

Query Match 100.0%; Score 4145; DB 41; Length 4145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
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Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
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Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
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Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
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Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
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Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
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Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
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Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
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Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
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Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
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Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
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Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
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Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy    3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy    3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy    3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy    3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy    3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy    3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy    4141 TAATC 4145
           |||||
Db    4141 TAATC 4145
```

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RESULT 14
US-09-543-679A-3017
; Sequence 3017, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3017:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 8222 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3017:
US-09-543-679A-3017

  Query Match           100.0%;  Score 4145;  DB 21;  Length 8222;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
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Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
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Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
```

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RESULT 15
US-09-543-679A-2509
; Sequence 2509, Application US/09543679A
;   GENERAL INFORMATION:
;        APPLICANT: NYCE, Jonathan W.
;        TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;                            COMPOSITIONS, KIT & METHOD FOR TREATMENT
;                            OF AIRWAY DISORDERS ASSOCIATED WITH
;                            BRONCHOCONSTRICTION, LUNG INFLAMMATION,
;        NUMBER OF SEQUENCES: 3111
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;             STREET: 7 Clarke Drive
;             CITY: Cranbury
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08512
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD-R
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: N/A
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/543,679A
;             FILING-DATE: 13-Apr-2000
;             CLASSIFICATION: UNKNOWN
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/127,958
;             FILING DATE: 1998-08-03
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amzel, Viviana
;             REGISTRATION NUMBER: 30,930
;             REFERENCE/DOCKET NUMBER: EPI-0067191b
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 609-409-3035
;             TELEFAX: 413-254-9245
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2509:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9513 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2509:
US-09-543-679A-2509

  Query Match             100.0%;  Score 4145;  DB 21;  Length 9513;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1292 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 1351

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1352 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 1411

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1412 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 1471

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1472 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 1531

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1532 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 1591

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1592 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 1651

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1652 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 1711

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1712 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 1771

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1772 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 1831

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1832 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 1891

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1892 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 1951

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1952 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 2011

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2012 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 2071

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2072 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 2131

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2132 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 2191

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2192 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 2251

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2252 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 2311

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2312 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 2371

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2372 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 2431

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2432 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 2491

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2492 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 2551

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2552 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 2611

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2612 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 2671

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2672 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 2731

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2732 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 2791

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2792 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 2851

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2852 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 2911

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2912 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 2971

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2972 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 3031

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3032 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 3091

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3092 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 3151

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3152 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 3211

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3212 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 3271

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3272 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 3331

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3332 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 3391

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3392 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 3451

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3452 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 3511

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3512 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 3571

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3572 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 3631

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3632 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 3691

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3692 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 3751
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Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3752 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 3811

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3812 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 3871

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3872 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 3931

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3932 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 3991

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3992 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 4051

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4052 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 4111

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4112 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 4171

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4172 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 4231

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4232 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 4291

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4292 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 4351

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4352 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 4411

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4412 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 4471

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4472 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 4531

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4532 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 4591

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4592 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 4651

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4652 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 4711

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4712 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 4771

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4772 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 4831

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4832 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 4891

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4892 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 4951

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4952 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 5011

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5012 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 5071

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5072 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 5131

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5132 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 5191

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5192 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 5251

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5252 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 5311

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
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Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
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Qy   4141 TAATC 4145
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Db   5432 TAATC 5436
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Search completed: March 14, 2003, 15:55:55
Job time : 8519 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 10:17:33 ; Search time 943 Seconds
(without alignments)
9987.245 Million cell updates/sec

Title: US-09-490-208-3
Perfect score: 4145
Sequence: 1 ctgctttaaaatctctcggc.....aattgcattttactttaatc 4145

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4666902 seqs, 1136064160 residues

Word size : 50

Total number of hits satisfying chosen parameters: 36

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending_Patents_NA_New:*
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9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3381	81.6	4062	8	US-10-305-720-1478	Sequence 1478, Ap
2	3047	73.5	3678	8	US-10-049-428-3	Sequence 3, Appli
3	3039	73.3	3855	8	US-10-210-682-1	Sequence 1, Appli
4	3039	73.3	3855	8	US-10-126-052A-312	Sequence 312, App
5	2906	70.1	3984	6	US-09-724-676-37685	Sequence 37685, A
6	2906	70.1	3984	6	US-09-724-676A-37685	Sequence 37685, A
7	2906	70.1	3985	6	US-09-724-676-37684	Sequence 37684, A
8	2906	70.1	3985	6	US-09-724-676A-37684	Sequence 37684, A
9	2769	66.8	4131	9	US-60-443-566-292	Sequence 292, App
10	2287	55.2	4062	6	US-09-724-676-37686	Sequence 37686, A
11	2287	55.2	4062	6	US-09-724-676A-37686	Sequence 37686, A
12	1769	42.7	3867	6	US-09-724-676-37688	Sequence 37688, A
13	1769	42.7	3867	6	US-09-724-676A-37688	Sequence 37688, A
14	1769	42.7	3868	6	US-09-724-676-37687	Sequence 37687, A
15	1769	42.7	3868	6	US-09-724-676A-37687	Sequence 37687, A
16	779	18.8	1049	6	US-09-724-676-37689	Sequence 37689, A
17	779	18.8	1049	6	US-09-724-676A-37689	Sequence 37689, A
18	619	14.9	1048	6	US-09-724-676-37682	Sequence 37682, A
19	619	14.9	1048	6	US-09-724-676A-37682	Sequence 37682, A
20	504	12.2	854	6	US-09-724-676-37683	Sequence 37683, A
21	504	12.2	854	6	US-09-724-676A-37683	Sequence 37683, A
22	344	8.3	853	6	US-09-724-676-37681	Sequence 37681, A
23	344	8.3	853	6	US-09-724-676A-37681	Sequence 37681, A
24	150	3.6	201	9	US-60-443-566-7053	Sequence 7053, Ap
25	150	3.6	201	9	US-60-443-566-7054	Sequence 7054, Ap
26	150	3.6	201	9	US-60-443-566-7055	Sequence 7055, Ap
27	150	3.6	201	9	US-60-443-566-7057	Sequence 7057, Ap
28	150	3.6	201	9	US-60-443-566-7061	Sequence 7061, Ap
29	150	3.6	201	9	US-60-443-566-7062	Sequence 7062, Ap
30	105	2.5	201	9	US-60-443-566-7058	Sequence 7058, Ap
31	100	2.4	201	9	US-60-443-566-7056	Sequence 7056, Ap
32	100	2.4	201	9	US-60-443-566-7059	Sequence 7059, Ap
33	100	2.4	201	9	US-60-443-566-7060	Sequence 7060, Ap
c 34	69	1.7	22345	6	US-09-949-002-681	Sequence 681, App
c 35	69	1.7	22345	6	US-09-949-002-746	Sequence 746, App
c 36	69	1.7	22347	6	US-09-949-002-745	Sequence 745, App

ALIGNMENTS

RESULT 1
US-10-305-720-1478
; Sequence 1478, Application US/10305720
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expres
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1478
; LENGTH: 4062
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No: g951320
US-10-305-720-1478

Query Match 81.6%; Score 3381; DB 8; Length 4062;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4031; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy    102 TACCCCGGGGAGGCAGTGCAGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAA 161
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Db      1 TACCCCGGGGAGGCAGTGCAGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAA 60

Qy    162 ATCCAGATAAGTGACATAAGTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGG 221
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Db     61 ATCCAGATAAGTGACATAAGTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGG 120

Qy    222 AAATTTCTGTTCAAGACCAAATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAAC 281
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Qy    282 AACAATGTGGAGAAAGCCCCCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAG 341
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Qy    342 TATCACAACCTCAGCAAGCAGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAG 401
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Qy    402 AAGTCTCCAGAATCTCTGGTCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTG 461
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Qy    462 AGGATCAAAAACTGGGGCAGCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAA 521
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Qy    522 GGGATTTTAACTTGCAGGTCCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTG 581
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Db    421 GGGATTTTAACTTGCAGGTCCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTG 480
Qy    582 ACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAA 641
Db    481 ACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAA 540
Qy    642 TTTGTCAACCAATATTACGGCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGG 701
Db    541 TTTGTCAACCAATATTACGGCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGG 600
Qy    702 GTGGAAGCGGTAACAAAGGAGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAG 761
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Qy   1302 GGGTGCCCCTTCAATGGCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGAC 1361
Db   1201 GGGTGCCCCTTCAATGGCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGAC 1260
Qy   1362 GTCCAGCGCTACAACATCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAG 1421
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Qy   1422 CTGGCCTCGCTCTGGAAAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGT 1481
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Qy   1542 TACATGCAGAATGAATACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTC 1601
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Qy   1662 TCCCCTTTCTACTACTATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAG 1721
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Qy   1842 GAGACAGGAAAATCAGAGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTC 1901
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Qy   1902 AACCCCAAGGTTGTCTGCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTG 1961
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Qy   1962 CTGTTGGTGGTGACCAGTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTG 2021
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Qy   2022 AAGAAATCGCTCTTCATGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGC 2081
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Qy   2202 GAGGACGCCTTCCGCAGCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGAT 2261
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Qy   2322 CCGCACCACTACAGGCTCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGC 2381
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Qy   2562 GGCATCCTGGAGCGAGTGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGAC 2621
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Qy   2682 CAGGCCCTCACCTACTCCCCGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAG 2741
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Qy   2742 CTGGCCCAGGTGGCCACAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCC 2801
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Qy   2802 TCAGAGTACAGCAAGTGGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAG 2861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TCAGAGTACAGCAAGTGGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAG 2760

Qy   2862 TTCCCGTCCCTGCGGGTGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCC 2921
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Qy   2922 AGGTTCTACTCCATCAGCTCCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTG 2981
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Qy   2982 GCCGTGGTCACCTACCACACCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGC 3041
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Db   2881 GCCGTGGTCACCTACCACACCGAGATGGCCAGGGTCCCCTGCACCACGGCGTCTGCAGC 2940

Qy   3042 ACATGGCTCAACAGCCTGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGC 3101
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Qy   3102 GCCTTCCACCTCCCCGAGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGC 3161
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Qy   3162 ATCGTGCCCTTCCGCAGTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTG 3221
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Qy   3222 CGGGGAGGCCGCATGACCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTAC 3281
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Db   3121 CGGGGAGGCCGCATGACCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTAC 3180

Qy   3282 CAGGAGGAGATGCTGGAGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTAT 3341
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Qy   3342 TCCCGCCTGCCTGGCAAGCCCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCC 3401
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Qy   3462 CGCATGGCCCGGGACGTGGCCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTG 3521
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Qy   3522 AATGAGGAGCAGGTCGAGGACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAA 3581
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Qy   3582 GATATCTTCGGTGCTGTATTTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCC 3641
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Qy   3822 TTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGG 3881
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTA 4020

Qy   4122 CATGAATTGCATTTTACTTTAATC 4145
          |||||||||||||||||||||||||
Db   4021 CATGAATTGCATTTTACTTTAATC 4044
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RESULT 2
US-10-049-428-3
; Sequence 3, Application US/10049428
; GENERAL INFORMATION:
; APPLICANT: Charles, Ian G.
; APPLICANT: Xu, Weiming
; APPLICANT: Liu, Lizhi
; TITLE OF INVENTION: Unducible Screen for Drug Discovery
; FILE REFERENCE: HO-P02380US0
; CURRENT APPLICATION NUMBER: US/10/049,428
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: GB 9918077
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: GB 0016171.1
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Human
US-10-049-428-3

Query Match 73.5%; Score 3047; DB 8; Length 3678;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3647; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     20 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 79

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     80 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 139

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    140 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 199

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    200 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 259

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    260 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 319

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    320 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 379

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    380 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 439

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    440 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 499

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    500 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 559

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    560 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 619

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    620 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 679

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    680 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 739

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    740 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 799

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    800 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 859

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    860 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 919

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    920 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 979

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    980 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1039

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1040 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1099

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1100 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1159

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1160 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1219

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1220 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1279

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1280 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1339

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1340 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1399

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1400 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1459
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Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          |||||||||||||||||||||||||||||||| ||||||||| ||||||||||||||||
Db   1460 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATGTGA 1519

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1520 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1579

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1580 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1639

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1640 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1699

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1700 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1759

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1760 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1819

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1820 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1879

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1880 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1939

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1940 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1999

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2000 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2059

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2060 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2119

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2120 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2179

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2180 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2239

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2240 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2299

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2300 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2359

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2360 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2419

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2420 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2479

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2480 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2539
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Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   2540 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGTATCCTGGAGCGAGTGG 2599

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   2600 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCT 2659

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   2660 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTTCC 2719

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2720 TGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2779

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2780 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2839

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2840 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2899

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2900 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2959

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   2960 CCTCCCGGGATCACACGCCCACAGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3019

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          || |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   3020 CCCGAGATGGCCAGGGTCCCCTGCACCACGGCGTCTGCAGCACATGGCTCAACAGCCTGA 3079

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   3080 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGGCTTCCACCTCCCCGAGG 3139

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   3140 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCAGTT 3199

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3200 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3259

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3260 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3319

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3320 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3379

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3380 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3439

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3440 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3499

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3500 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3559

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   3560 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTTGGTGCTGTAT 3619

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCA 3659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3620 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCA 3678
```

RESULT 3
US-10-210-682-1
; Sequence 1, Application US/10210682
; GENERAL INFORMATION:
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Donald, Glen
; TITLE OF INVENTION: Screening Nutraceuticals
; FILE REFERENCE: FORS-07289
; CURRENT APPLICATION NUMBER: US/10/210,682
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/309,279
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3855
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-210-682-1

Query Match 73.3%; Score 3039; DB 8; Length 3855;
Best Local Similarity 80.1%; Pred. No. 0;
Matches 3086; Conservative 753; Mismatches 16; Indels 0; Gaps 0;

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Qy     13 CTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCGAAGTTCTCAAGG 72
          |:|:|||||||:::||:|||||||:||||||::|:||||||:||||||::|:|||||
Db      1 CUCUCGGCCACCUUUGAUGAGGGGACUGGGCAGUUCUAGACAGUCCCGAAGUUCUCAAGG 60

Qy     73 CACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGCAGCCAGCTGCAA 132
          ||||||:|:|::||:||:::|||:|:||::|||||||||||||||||||:|||||
Db     61 CACAGGUCUCUUCCUGGUUUGACUGUCCUUACCCCGGGGAGGCAGUGCAGCCAGCUGCAA 120

Qy    133 GCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAAGTGACCTGCTTT 192
          |||||||||:||||||||:|:||||:||||:|||||:|||:||||:|||:|||||:||:::
Db    121 GCCCCACAGUGAAGAACAUCUGAGCUCAAAUCCAGAUAAGUGACAUAAGUGACCUGCUUU 180

Qy    193 GTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCAGT 252
          |:||||||:|||||:||||:|:||::|||||:::|:|::||||||||||::|||||||:
Db    181 GUAAAGCCAUAGAGAUGGCCUGUCCUUGGAAAUUUCUGUUCAAGACCAAAUUCCACCAGU 240

Qy    253 ATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCCCCTGTGCCACCT 312
          |:||||:|||:||||||||| ||:|||||||||:|:||||||||||||:|:|||||||:
Db    241 AUGCAAUGAAUGGGGAAAAAGGCAUCAACAACAAUGUGGAGAAAGCCCCCUGUGCCACCU 300

Qy    313 CCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGAGT 372
          ||||:||||:|||||||||:||||::|||:|:||||||||:|||||||||||||||:|||:
Db    301 CCAGUCCAGUGACACAGGAUGACCUUCAGUAUCACAACCUCAGCAAGCAGCAGAAUGAGU 360

Qy    373 CCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGATG 432
          |||||||||||:||:|||||||||||||:|:|||||:|:|:||:|||||:|||:|
Db    361 CCCCGCAGCCCCUCGUGGAGACGGGAAAGAAGUCUCCAGAAUCUCUGGUCAAGCUGGAUG 420

Qy    433 CAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGACTT 492
          |||||||::|:||:|||||||:|||||||:|||||||:||||||||||:|||::
Db    421 CAACCCCAUUGUCCUCCCCACGGCAUGUGAGGAUCAAAAACUGGGGCAGCGGGAUGACUU 480

Qy    493 TCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTGCC 552
          :|||||||||||::|||||:|||||||||||||:::|||::|||||:|||||:|::|||
Db    481 UCCAAGACACACUUCACCAUAAGGCCAAAGGGAUUUUAACUUGCAGGUCCAAAUCUUGCC 540

Qy    553 TGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTC 612
          :||||:|||::|:|||:|||||||||:::|||||||||||||||||||||||:|||||:|
Db    541 UGGGGUCCAUUAUGACUCCCAAAAGUUUGACCAGAGGACCCAGGGACAAGCCUACCCCUC 600

Qy    613 CAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCTTCAAAG 672
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Db    601 CAGAUGAGCUUCUACCUCAAGCUAUCGAAUUUGUCAACCAAUAUUACGGCUCCCUCAAAG 660

Qy    673 AGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAACAA 732
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Qy   2893 TGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCTCCTCCCGGGATC 2952
Db   2881 UGCUUUCCCAGCUCCCCAUUCUGAAGCCCAGGUUCUACUCCAUCAGCUCCCCCCGGGAUC 2940

Qy   2953 ACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACACCGGAGATGGCC 3012
Db   2941 ACACGCCCACGGAGAUCCACCUGACUGUGGCCGUGGUCACCUACCACACCCGAGAUGGCC 3000

Qy   3013 AGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGAAGCCCCAAGACC 3072
Db   3001 AGGGUCCCCUGCACCACGGCGUCUGCAGCACAUGGCUCAACAGCCUGAAGCCCCAAGACC 3060

Qy   3073 CAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGGATCCCTCCCATC 3132
Db   3061 CAGUGCCCUGCUUUGUGCGGAAUGCCAGCGGCUUCCACCUCCCCGAGGAUCCCUCCCAUC 3120

Qy   3133 CTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTTTCTGGCAGCAAC 3192
Db   3121 CUUGCAUCCUCAUCGGGCCUGGCACAGGCAUCGCGCCCUUCCGCAGUUUCUGGCAGCAAC 3180

Qy   3193 GGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCTTGGTGTTTGGGT 3252
Db   3181 GGCUCCAUGACUCCCAGCACAAGGGAGUGCGGGGAGGCCGCAUGACCUUGGUGUUUGGGU 3240

Qy   3253 GCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGATGGCCCAGAAGG 3312
Db   3241 GCCGCCGCCCAGAUGAGGACCACAUCUACCAGGAGGAGAUGCUGGAGAUGGCCCAGAAGG 3300

Qy   3313 GGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGCCCAAGGTCTATG 3372
Db   3301 GGGUGCUGCAUGCGGUGCACACAGCCUAUUCCCGCCUGCCUGGCAAGCCCAAGGUCUAUG 3360

Qy   3373 TTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGCTCCACAAGGAGC 3432
Db   3361 UUCAGGACAUCCUGCGGCAGCAGCUGGCCAGCGAGGUGCUCCGUGUGCUCCACAAGGAGC 3420

Qy   3433 CAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGGCCCACACCCTGA 3492
Db   3421 CAGGCCACCUCUAUGUUUGCGGGGAUGUGCGCAUGGCCCGGGACGUGGCCCACACCCUGA 3480

Qy   3493 AGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGGACTATTTCTTTC 3552
Db   3481 AGCAGCUGGUGGCUGCCAAGCUGAAAUUGAAUGAGGAGCAGGUCGAGGACUAUUUCUUUC 3540

Qy   3553 AGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTATTTCCTTACGAGG 3612
Db   3541 AGCUCAAGAGCCAGAAGCGCUAUCACGAAGAUAUCUUUGGUGCUGUAUUUCCUUACGAGG 3600

Qy   3613 CGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAGCGCTCTGAGGGC 3672
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Qy   3673 CTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTAT 3732
Db   3661 CUACAGGAGGGGUUAAAGCUGCCGGCACAGAACUUAAGGAUGGAGCCAGCUCUGCAUUAU 3720

Qy   3733 CTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTAT 3792
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Qy   3793 TTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGG 3852
Db   3781 UUCCUCAACGUUGCUCCCCAUCAAGCCCUUUACUUGACCUCCUAACAAGUAGCACCCUGG 3840

Qy   3853 ATTGATCGGAGCCTC 3867
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RESULT 4
US-10-126-052A-312
; Sequence 312, Application US/10126052A
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Lung Cancer
;  FILE REFERENCE: 018501-001530US
;  CURRENT APPLICATION NUMBER: US/10/126,052A
;  CURRENT FILING DATE:  2002-04-18
;  PRIOR APPLICATION NUMBER: US 60/284,770
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: US 60/290,492
;  PRIOR FILING DATE: 2001-05-10
;  PRIOR APPLICATION NUMBER: US 60/339,245
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/334,370
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/372,246
;  PRIOR FILING DATE: 2002-04-12
;  NUMBER OF SEQ ID NOS: 691
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 312
;   LENGTH: 3855
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-126-052A-312

  Query Match             73.3%;  Score 3039;  DB 8;  Length 3855;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 3839;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy     13 CTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCGAAGTTCTCAAGG 72
Db      1 CTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCGAAGTTCTCAAGG 60

Qy     73 CACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGCAGCCAGCTGCAA 132
Db     61 CACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGCAGCCAGCTGCAA 120

Qy    133 GCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAAGTGACCTGCTTT 192
Db    121 GCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAAGTGACCTGCTTT 180

Qy    193 GTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCAGT 252
Db    181 GTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCAGT 240

Qy    253 ATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCCCCTGTGCCACCT 312
Db    241 ATGCAATGAATGGGGAAAAAGGCATCAACAACAATGTGGAGAAAGCCCCCTGTGCCACCT 300

Qy    313 CCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGAGT 372
Db    301 CCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGAGT 360

Qy    373 CCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGATG 432
Db    361 CCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGATG 420

Qy    433 CAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGACTT 492
Db    421 CAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGACTT 480

Qy    493 TCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTGCC 552
Db    481 TCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTGCC 540

Qy    553 TGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTC 612
Db    541 TGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTC 600
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Qy    613 CAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCTTCAAAG 672
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Db    601 CAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCCTCAAAG 660

Qy    673 AGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAACAA 732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAACAA 720

Qy    733 CAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCA 792
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAGTAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCA 780

Qy    793 ATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCGCA 852
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Db    781 ATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCGCA 840

Qy    853 GCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCACCA 912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCACCA 900

Qy    913 ACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCACG 972
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Db    901 ACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCACG 960

Qy    973 ACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCA 1032
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Db    961 ACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCA 1020

Qy   1033 GCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCGACCTGGGCTGGA 1092
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Qy   1093 AGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGACC 1152
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Db   1081 AGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGACC 1140

Qy   1153 CTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAAAT 1212
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Db   1141 CTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAAAT 1200

Qy   1213 ACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACATGC 1272
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Db   1201 ACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACATGC 1260

Qy   1273 TGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGGCA 1332
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Db   1261 TGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGGCA 1320

Qy   1333 CAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCCTGGAGGAAGTGG 1392
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1321 CAGAGATCGGAGTCCGGGACTTCTGTGATGTCCAGCGCTACAACATCCTGGAGGAAGTGG 1380

Qy   1393 GCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGTCG 1452
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Db   1381 GCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGTCG 1440

Qy   1453 TTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGACCATCATGGACC 1512
          |||||||||||||||||||| |||||||||| ||||||||||||||||||||||||||||||
Db   1441 TTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATGTGACCATCATGGACC 1500

Qy   1513 ACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGGGG 1572
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Db   1501 ACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGGGG 1560

Qy   1573 GCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGTGT 1632
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Db   1561 GCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGTGT 1620

Qy   1633 TTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGCCT 1692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGCCT 1680

Qy   1693 GGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAGAGATTCCATTGA 1752
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Db   1681 GGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAGAGATTCCATTGA 1740

Qy   1753 AAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGACAATGGCGTCCC 1812
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Qy   1813 GAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGGCGCTGGCCTGGG 1872
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Qy   1873 ACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCATGGATAAGTACA 1932
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Db   1861 ACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCATGGATAAGTACA 1920

Qy   1933 GGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTACGTTTGGCAATG 1992
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Db   1921 GGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTACGTTTGGCAATG 1980

Qy   1993 GAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGCTGAAAGAGCTCA 2052
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Db   1981 GAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGCTGAAAGAGCTCA 2040

Qy   2053 ACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACCCTCGGTTCTGCG 2112
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Db   2041 ACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACCCTCGGTTCTGCG 2100

Qy   2113 CCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTCAGCTCACCCCGA 2172
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Db   2101 CCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTCAGCTCACCCCGA 2160

Qy   2173 TGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCTGGGCCGTGCAAA 2232
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Qy   2233 CCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACATTCAGATCCCCA 2292
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Qy   2293 AGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCGTGCAGGACTCAC 2352
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Db   2281 AGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCGTGCAGGACTCAC 2340

Qy   2353 AGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCATGA 2412
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Qy   2413 GGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGTGG 2472
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Db   2401 GGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGTGG 2460

Qy   2473 AACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGGAGCACCTTGGGGTTT 2532
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Qy   2533 GCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGGTGGATGGCCCCA 2592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2593 CACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCTACTGGGTCAGTG 2652
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Db   2581 CACCCCACCAGGCAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCTACTGGGTCAGTG 2640

Qy   2653 ACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCCCGGACATCACCA 2712
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Qy   2713 CACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAGAAGAGCCTGAGA 2772
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Qy   2773 GACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGAAGTTCACCAACA 2832
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Qy   3073 CAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGGATCCCTCCCATC 3132
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Qy   3253 GCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGATGGCCCAGAAGG 3312
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Db   3241 GCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGATGGCCCAGAAGG 3300

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Db   3301 GGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGCCCAAGGTCTATG 3360

Qy   3373 TTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGCTCCACAAGGAGC 3432
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Db   3361 TTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGCTCCACAAGGAGC 3420

Qy   3433 CAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGGCCCACACCCTGA 3492
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Db   3421 CAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGGCCCACACCCTGA 3480

Qy   3493 AGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGGACTATTTCTTTC 3552
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Db   3481 AGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGGACTATTTCTTTC 3540

Qy   3553 AGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTATTTCCTTACGAGG 3612
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Qy   3613 CGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAGCGCTCTGAGGGC 3672
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Qy   3673 CTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTAT 3732
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Db   3661 CTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTAT 3720

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Db   3721 CTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTAT 3780

Qy   3793 TTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGG 3852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGG 3840

Qy   3853 ATTGATCGGAGCCTC 3867
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Db   3841 ATTGATCGGAGCCTC 3855
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RESULT 5
US-09-724-676-37685
; Sequence 37685, Application US/09724676
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37685
;   LENGTH: 3984
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676-37685

  Query Match             70.1%;  Score 2906;  DB 6;  Length 3984;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 3356;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 88

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      89 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 148

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 208

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     209 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 268

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     269 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 328

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     329 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 388

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     389 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 448

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     449 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 508

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     509 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 568

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     569 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 628

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     629 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 688

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     689 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 748

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
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Db    749 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 808

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    809 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 868

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    869 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 928

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    929 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 988

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    989 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1048

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1049 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1108

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1168

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1169 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1228

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1229 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1288

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1289 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1348

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1349 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1408

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1409 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1468

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          |||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||
Db   1469 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATGTGA 1528

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1529 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1588

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1589 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1648

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1649 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1708

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1709 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1768

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1769 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1828

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
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Db   1829 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1888

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1889 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1948

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1949 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 2008

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2068

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2069 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2128

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2129 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2188

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
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Db   2189 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2248

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2249 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2308

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2309 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2368

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2369 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2428

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2429 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2488

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
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Db   2489 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2548

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2549 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2608

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   2609 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCT 2668

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   2669 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTTCC 2728

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2729 TGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2788

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2789 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2848

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2849 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2908

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2909 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2968
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Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
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Db   2969 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3028

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          || ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   3029 CCCGAGATGGCCAGGGTCCCCTGCACCACGGCGTCTGCAGCACATGGCTCAACAGCCTGA 3088

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   3089 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGGCTTCCACCTCCCCGAGG 3148

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
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Db   3149 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCAGTT 3208

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3209 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3268

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
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Db   3269 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3328

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3329 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3388

Qy   3361 CCAAG 3365
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Db   3389 CCAAG 3393
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RESULT 6
US-09-724-676A-37685
; Sequence 37685, Application US/09724676A
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676A
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37685
;   LENGTH: 3984
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676A-37685

  Query Match             70.1%;  Score 2906;  DB 6;  Length 3984;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 3356;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     29 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 88

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 148

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
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Db    149 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 208

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
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Db    209 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 268

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
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Db    269 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 328
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Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
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Db    329 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 388

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    389 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 448

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    449 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 508

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
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Db    509 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 568

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
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Db    569 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 628

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
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Db    629 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 688

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    689 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 748

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    749 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 808

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    809 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 868

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
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Db    869 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 928

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    929 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 988

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    989 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1048

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1049 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1108

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
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Db   1109 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1168

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1169 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1228

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
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Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
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Db   1289 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1348

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
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Db   1409 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1468

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Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
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Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
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Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
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Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
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Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
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Db   1949 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 2008

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
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Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
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Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
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Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
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Db   2249 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2308

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
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Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
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Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
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Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
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Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
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Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
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RESULT 7
US-09-724-676-37684
; Sequence 37684, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28

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;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37684
;   LENGTH: 3985
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676-37684

  Query Match             70.1%;  Score 2906;  DB 6;  Length 3985;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 3356;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

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Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
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Qy    2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
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Db    2069 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2128

Qy    2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2129 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2188

Qy    2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2189 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2248

Qy    2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2249 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2308

Qy    2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2309 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2368

Qy    2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2369 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2428

Qy    2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2429 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2488

Qy    2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2489 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2548

Qy    2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2549 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2608

Qy    2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    2609 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCT 2668

Qy    2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    2669 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTTCC 2728

Qy    2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2729 TGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2788

Qy    2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2789 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2848

Qy    2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2849 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2908

Qy    2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2909 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2968

Qy    2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2969 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3028

Qy    3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
           || ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    3029 CCCGAGATGGCCAGGGTCCCCTGCACCACGGCGTCTGCAGCACATGGCTCAACAGCCTGA 3088

Qy    3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
           ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
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Qy    3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    3149 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCAGTT 3208

Qy    3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3209 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3268

Qy    3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
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Db    3269 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3328

Qy    3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
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Db    3329 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3388

Qy    3361 CCAAG 3365
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Db    3389 CCAAG 3393
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RESULT 8
US-09-724-676A-37684
; Sequence 37684, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37684
; LENGTH: 3985
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-37684

Query Match 70.1%; Score 2906; DB 6; Length 3985;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3356; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
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Db      29 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 88

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      89 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 148

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 208

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     209 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 268

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
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Db     269 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 328

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     329 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 388

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     389 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 448

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    449 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 508

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
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Db    509 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 568

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
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Db    569 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 628

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
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Db    629 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 688

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    689 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 748

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    749 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 808

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
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Db    809 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 868

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
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Db    869 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 928

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
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Db    929 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 988

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    989 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1048

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
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Db   1049 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1108

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
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Db   1109 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1168

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
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Db   1169 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1228

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
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Db   1229 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1288

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1289 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1348

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1349 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1408

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1409 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1468

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||||||
Db   1469 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATGTGA 1528

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
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Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
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Db   1589 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1648

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1649 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1708

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1709 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1768

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
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Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
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Db   1829 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1888

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
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Db   1889 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1948

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
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Db   1949 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 2008

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
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Db   2009 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2068

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
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Db   2069 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2128

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Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
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Db   2189 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2248

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
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Db   2309 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2368

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
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Db   2369 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2428

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
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Db   2429 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2488

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
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Db   2489 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2548

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
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Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
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Db   2609 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCT 2668
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Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   2669 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTTCC 2728

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Db   2789 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2848

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Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3149 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCAGTT 3208

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3209 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3268

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3269 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3328

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3329 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3388

Qy   3361 CCAAG 3365
          |||||
Db   3389 CCAAG 3393
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RESULT 9
US-60-443-566-292
; Sequence 292, Application US/60443566
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001447
; CURRENT APPLICATION NUMBER: US/60/443,566
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 25102
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292
; LENGTH: 4131
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-443-566-292

Query Match 66.8%; Score 2769; DB 9; Length 4131;

Best Local Similarity 99.4%; Pred. No. 0;
Matches 4109; Conservative 0; Mismatches 22; Indels 2; Gaps 2;

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Qy     13 CTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCGAAGTTCTCAAGG 72
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCGAAGTTCTCAAGG 60

Qy     73 CACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGCAGCCAGCTGCAA 132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGCAGCCAGCTGCAA 120

Qy    133 GCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAAGTGACCTGCTTT 192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAAGTGACCTGCTTT 180

Qy    193 GTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCAGT 252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCAGT 240

Qy    253 ATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCCCCTGTGCCACCT 312
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    241 ATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCYCCCTGTGCCACCT 300

Qy    313 CCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGAGT 372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGAGT 360

Qy    373 CCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGATG 432
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    361 CCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCRGAATCTCTGGTCAAGCTGGATG 420

Qy    433 CAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGACTT 492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGACTT 480

Qy    493 TCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTGCC 552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTGCC 540

Qy    553 TGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTC 612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTC 600

Qy    613 CAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCTTCAAAG 672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCTTCAAAG 660

Qy    673 AGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAACAA 732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAACAA 720

Qy    733 CAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCA 792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCA 780

Qy    793 ATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCGCA 852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCGCA 840

Qy    853 GCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCACCA 912
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCTGTTCCACTGCCYGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCACCA 900

Qy    913 ACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCACG 972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCACG 960

Qy    973 ACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCA 1032
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCA 1020

Qy   1033 GCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCGACCTGGGCTGGA 1092
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1021 GCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCGACCTGGGCTGGA 1080
Qy  1093 AGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGACC 1152
Db  1081 AGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGACC 1140
Qy  1153 CTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAAAT 1212
Db  1141 CTGAGCTCTTYGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAAAT 1200
Qy  1213 ACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACATGC 1272
Db  1201 ACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACATGC 1260
Qy  1273 TGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGGCA 1332
Db  1261 TGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGGCA 1320
Qy  1333 CAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCCTGGAGGAAGTGG 1392
Db  1321 CAGAGATCGGAGTCCGGGACTTCTGTGAYGTCCAGCGCTACAACATCCTGGAGGAAGTGG 1380
Qy  1393 GCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGTCG 1452
Db  1381 GCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGTCG 1440
Qy  1453 TTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGACCATCATGGACC 1512
Db  1441 TTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATGTGACCATCATGGACC 1500
Qy  1513 ACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGGGG 1572
Db  1501 ACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGGGG 1560
Qy  1573 GCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGTGT 1632
Db  1561 GCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGTGT 1620
Qy  1633 TTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGCCT 1692
Db  1621 TTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGCCT 1680
Qy  1693 GGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAGAGATTCCATTGA 1752
Db  1681 GGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAGAGATTCCATTGA 1740
Qy  1753 AAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGACAATGGCGTCCC 1812
Db  1741 AAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGACAATGGCGTCCC 1800
Qy  1813 GAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGGCGCTGGCCTGGG 1872
Db  1801 GAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGGCGCTGGCCTGGG 1860
Qy  1873 ACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCATGGATAAGTACA 1932
Db  1861 ACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCATGGATAAGTACA 1920
Qy  1933 GGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTACGTTTGGCAATG 1992
Db  1921 GGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTACGTTTGGCAATG 1980
Qy  1993 GAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGCTGAAAGAGCTCA 2052
Db  1981 GAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATYGCTCTTCATGCTGAAAGAGCTCA 2040
Qy  2053 ACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACCCTCGGTTCTGCG 2112
Db  2041 ACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACCCTCGGTTCTGCG 2100
Qy  2113 CCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTCAGCTCACCCCGA 2172
Db  2101 CCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTCAGCTCACCCCGA 2160

Qy  2173 TGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCTGGGCCGTGCAAA 2232
Db  2161 TGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCTGGGCCGTGCAAA 2220
Qy  2233 CCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACATTCAGATCCCCA 2292
Db  2221 CCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACATTCAGATCCCCA 2280
Qy  2293 AGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCGTGCAGGACTCAC 2352
Db  2281 AGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCGTGCAGGACTCAC 2340
Qy  2353 AGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCATGA 2412
Db  2341 AGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCATGA 2400
Qy  2413 GGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGTGG 2472
Db  2401 GGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGTGG 2460
Qy  2473 AACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGGAGCACCTTGGGGTTT 2532
Db  2461 AACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGGAGCACCTTGGGGTTT 2520
Qy  2533 GCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGGTGGATGGCCCCA 2592
Db  2521 GCCCAGGCAACCAGCCGGCCCTGGTCCAAGGYATCCTGGAGCGAGTGGTGGATGGCCCCA 2580
Qy  2593 CACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCTACTGGGTCAGTG 2652
Db  2581 CACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCTACTGGGTCAGTG 2640
Qy  2653 ACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCCCGGACATCACCA 2712
Db  2641 ACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTTCCTGGACATCACCA 2700
Qy  2713 CACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAGAAGAGCCTGAGA 2772
Db  2701 CACCCCC-ACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAGAAAAGCCTGAGA 2759
Qy  2773 GACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGAAGTTCACCAACA 2832
Db  2760 GAC-GAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGAAGTTCACCAACA 2818
Qy  2833 GCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGTCTGCTGGCTTCC 2892
Db  2819 GCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGTCTGCTGGCTTCC 2878
Qy  2893 TGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCTCCTCCCGGGATC 2952
Db  2879 TGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCTCCTCCCGGGATC 2938
Qy  2953 ACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACACCGGAGATGGCC 3012
Db  2939 ACACGCCCACRGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACACCCGAGATGGCC 2998
Qy  3013 AGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGAAGCCCCAAGACC 3072
Db  2999 AGGGTCCCCTGCACCACGGCGTCTGCAGCACATGGCTCAACAGCCTGAAGCCCCAAGACC 3058
Qy  3073 CAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGGATCCCTCCCATC 3132
Db  3059 CAGTGCCCTGCTTTGTGCGGAATGCCAGCGGCTTCCACCTCCCCGAGGATCCCTCCCATC 3118
Qy  3133 CTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTTTCTGGCAGCAAC 3192
Db  3119 CTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCAGTTTCTGGCAGCAAC 3178
Qy  3193 GGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCTTGGTGTTTGGGT 3252
Db  3179 GGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCTTGGTGTTTGGGT 3238
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Qy   3253 GCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGATGGCCCAGAAGG 3312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3239 GCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGATGGCCCAGAAGG 3298

Qy   3313 GGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGCCCAAGGTCTATG 3372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3299 GGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGCCCAAGGTCTATG 3358

Qy   3373 TTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGCTCCACAAGGAGC 3432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3359 TTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGCTCCACAAGGAGC 3418

Qy   3433 CAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGGCCCACACCCTGA 3492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3419 CAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGGCCCACACCCTGA 3478

Qy   3493 AGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGGACTATTTCTTTC 3552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3479 AGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGGACTATTTCTTTC 3538

Qy   3553 AGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTATTTCCTTACGAGG 3612
          |||||||||||||||||||||||| |||||||||| ||||||||||||||||||||||||
Db   3539 AGCTCAAGAGCCAGAAGCGCTATCAYGAAGATATCTTTGGTGCTGTATTTCCTTACGAGG 3598

Qy   3613 CGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAGCGCTCTGAGGGC 3672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3599 CGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAGCGCTCTGAGGGC 3658

Qy   3673 CTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTAT 3732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3659 CTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTAT 3718

Qy   3733 CTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTAT 3792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3719 CTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTAT 3778

Qy   3793 TTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGG 3852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3779 TTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGG 3838

Qy   3853 ATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTT 3912
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   3839 ATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACRAAATCTT 3898

Qy   3913 AAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAA 3972
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   3899 AAATGCCAGGCCTGGCAAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAA 3958

Qy   3973 GTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATT 4032
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3959 GTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATT 4018

Qy   4033 TATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTC 4092
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4019 TATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTC 4078

Qy   4093 CCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTTTAATC 4145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4079 CCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTTTAATC 4131
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RESULT 10
US-09-724-676-37686
; Sequence 37686, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37686

; LENGTH: 4062
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-37686

Query Match 55.2%; Score 2287; DB 6; Length 4062;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2837; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy   1138 CCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCA 1197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1049 CCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCA 1108

Qy   1198 TGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTG 1257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109 TGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTG 1168

Qy   1258 CAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATG 1317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1169 CAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATG 1228

Qy   1318 GCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACA 1377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1229 GCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACA 1288

Qy   1378 TCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGA 1437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1289 TCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGA 1348

Qy   1438 AAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATG 1497
          |||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||
Db   1349 AAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATG 1408

Qy   1498 TGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAAT 1557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1409 TGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAAT 1468

Qy   1558 ACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGA 1617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1469 ACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGA 1528

Qy   1618 GCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACT 1677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1529 GCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACT 1588

Qy   1678 ATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAA 1737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1589 ATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAA 1648

Qy   1738 GAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCA 1797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1649 GAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCA 1708

Qy   1798 AGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAG 1857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1709 AGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAG 1768

Qy   1858 AGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCT 1917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1769 AGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCT 1828

Qy   1918 GCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCA 1977
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Db   1829 GCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCA 1888

Qy   1978 GTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCA 2037
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Db   1889 GTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATGGCTCTTCA 1948

Qy   2038 TGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGT 2097
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Qy   2098 ACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCT 2157
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Db   2009 ACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCT 2068

Qy   2158 CTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCA 2217
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Qy   2218 GCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGC 2277
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Db   2129 GCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGC 2188

Qy   2278 ACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGC 2337
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Qy   2338 TCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGA 2397
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Qy   2458 CCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGG 2517
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Qy   2518 AGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAG 2577
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Qy   2578 TGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCA 2637
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Qy   2818 GGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGG 2877
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Qy   3538 AGGACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTG 3597
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RESULT 11
US-09-724-676A-37686
; Sequence 37686, Application US/09724676A
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676A
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37686
;   LENGTH: 4062
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676A-37686
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Query Match 55.2%; Score 2287; DB 6; Length 4062;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2837; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy   3538 AGGACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTG 3597
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Db   3449 AGGACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTTGGTGCTG 3508

Qy   3598 TATTTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGT 3657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3509 TATTTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGT 3568

Qy   3658 CAGCGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAG 3717
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3569 CAGCGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAG 3628

Qy   3718 CCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCC 3777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3629 CCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCC 3688

Qy   3778 AGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAA 3837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3689 AGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAA 3748

Qy   3838 CAAGTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCT 3897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3749 CAAGTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCT 3808

Qy   3898 TGGAGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTG 3957
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   3809 TGGAGACAAAATCTTAAATGCCAGGCCTGGCAAGTGGGTGAAAGATGGAACTTGCTGCTG 3868

Qy   3958 AGTGCACCACTTCAAGTGACCACCAGGA 3985
          ||||||||||||||||||||||||||||
Db   3869 AGTGCACCACTTCAAGTGACCACCAGGA 3896


RESULT 12
US-09-724-676-37688
; Sequence 37688, Application US/09724676
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37688
;   LENGTH: 3867
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676-37688

  Query Match             42.7%;  Score 1769;  DB 6;  Length 3867;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2219;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   1138 CCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCA 1197
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Db   1049 CCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCA 1108

Qy   1198 TGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTG 1257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109 TGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTG 1168

Qy   1258 CAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATG 1317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1169 CAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATG 1228

Qy   1318 GCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACA 1377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1229 GCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACA 1288

Qy   1378 TCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGA 1437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1289 TCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGA 1348

Qy   1438 AAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATG 1497
          |||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||
Db   1349 AAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATG 1408

Qy   1498 TGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAAT 1557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1409 TGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAAT 1468

Qy   1558 ACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGA 1617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1469 ACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGA 1528

Qy   1618 GCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACT 1677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1529 GCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACT 1588

Qy   1678 ATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAA 1737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1589 ATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAA 1648

Qy   1738 GAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCA 1797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1649 GAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCA 1708

Qy   1798 AGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAG 1857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1709 AGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAG 1768

Qy   1858 AGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCT 1917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1769 AGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCT 1828

Qy   1918 GCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCA 1977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1829 GCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCA 1888

Qy   1978 GTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCA 2037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1889 GTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCA 1948

Qy   2038 TGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGT 2097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1949 TGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGT 2008

Qy   2098 ACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCT 2157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 ACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCT 2068

Qy   2158 CTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCA 2217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2069 CTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCA 2128

Qy   2218 GCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGC 2277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2129 GCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGC 2188

Qy   2278 ACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGC 2337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2189 ACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGC 2248

Qy   2338 TCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGA 2397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2249 TCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGA 2308

Qy   2398 ACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTG 2457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2309 ACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTG 2368

Qy   2458 CCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGG 2517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2369 CCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGG 2428

Qy   2518 AGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAG 2577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2429 AGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAG 2488

Qy   2578 TGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCA 2637
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   2489 TGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCA 2548

Qy   2638 GCTACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACT 2697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2549 GCTACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACT 2608

Qy   2698 CCCCGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCA 2757
            || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2609 TCCTGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCA 2668

Qy   2758 CAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGT 2817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2669 CAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGT 2728

Qy   2818 GGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGG 2877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2729 GGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGG 2788

Qy   2878 TGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCA 2937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2789 TGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCA 2848

Qy   2938 GCTCCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACC 2997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2849 GCTCCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACC 2908

Qy   2998 ACACCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCC 3057
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2909 ACACCCGAGATGGCCAGGGTCCCCTGCACCACGGCGTCTGCAGCACATGGCTCAACAGCC 2968

Qy   3058 TGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCG 3117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2969 TGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGGCTTCCACCTCCCCG 3028

Qy   3118 AGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCA 3177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3029 AGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCA 3088

Qy   3178 GTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGA 3237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3089 GTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGA 3148

Qy   3238 CCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGG 3297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3149 CCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGG 3208

Qy   3298 AGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCA 3357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3209 AGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCA 3268

Qy   3358 AGCCCAAG 3365
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Db   3269 AGCCCAAG 3276
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RESULT 13
US-09-724-676A-37688
; Sequence 37688, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37688
; LENGTH: 3867
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-37688

Query Match 42.7%; Score 1769; DB 6; Length 3867;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2219; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy   1138 CCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCA 1197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1049 CCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCA 1108

Qy   1198 TGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTG 1257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109 TGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTG 1168

Qy   1258 CAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATG 1317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1169 CAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATG 1228

Qy   1318 GCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACA 1377
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Db   1229 GCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACA 1288

Qy   1378 TCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGA 1437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1289 TCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGA 1348

Qy   1438 AAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATG 1497
          |||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||
Db   1349 AAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATG 1408

Qy   1498 TGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAAT 1557
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Db   1409 TGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAAT 1468

Qy   1558 ACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGA 1617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1469 ACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGA 1528

Qy   1618 GCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACT 1677
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Db   1529 GCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACT 1588

Qy   1678 ATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAA 1737
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Db   1589 ATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAA 1648

Qy   1738 GAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCA 1797
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Db   1649 GAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCA 1708

Qy   1798 AGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAG 1857
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Db   1709 AGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAG 1768

Qy   1858 AGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCT 1917
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Db   1769 AGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCT 1828

Qy   1918 GCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCA 1977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1829 GCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCA 1888

Qy   1978 GTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCA 2037
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Db   1889 GTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCA 1948

Qy   2038 TGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGT 2097
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Db   1949 TGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGT 2008

Qy   2098 ACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCT 2157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 ACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCT 2068

Qy   2158 CTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCA 2217
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Db   2069 CTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCA 2128

Qy   2218 GCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGC 2277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2129 GCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGC 2188

Qy   2278 ACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGC 2337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2189 ACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGC 2248

Qy   2338 TCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGA 2397
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Db   2249 TCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGA 2308

Qy   2398 ACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTG 2457
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Db   2309 ACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTG 2368

Qy   2458 CCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGG 2517
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Db   2369 CCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGG 2428

Qy   2518 AGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAG 2577
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Db   2429 AGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAG 2488

Qy   2578 TGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCA 2637
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Db   2489 TGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCA 2548

Qy   2638 GCTACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACT 2697
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Db   2549 GCTACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACT 2608

Qy   2698 CCCCGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCA 2757
           || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2609 TCCTGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCA 2668

Qy   2758 CAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGT 2817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2669 CAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGT 2728

Qy   2818 GGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGG 2877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2729 GGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGG 2788

Qy   2878 TGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCA 2937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2789 TGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCA 2848
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Qy   2938 GCTCCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACC 2997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2849 GCTCCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACC 2908

Qy   2998 ACACCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCC 3057
          ||||| |||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   2909 ACACCCGAGATGGCCAGGGTCCCCTGCACCACGGCGTCTGCAGCACATGGCTCAACAGCC 2968

Qy   3058 TGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCG 3117
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   2969 TGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGGCTTCCACCTCCCCG 3028

Qy   3118 AGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCA 3177
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   3029 AGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCA 3088

Qy   3178 GTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGA 3237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3089 GTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGA 3148

Qy   3238 CCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGG 3297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3149 CCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGG 3208

Qy   3298 AGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCA 3357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3209 AGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCA 3268

Qy   3358 AGCCCAAG 3365
          ||||||||
Db   3269 AGCCCAAG 3276
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RESULT 14
US-09-724-676-37687
; Sequence 37687, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37687
; LENGTH: 3868
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-37687

Query Match 42.7%; Score 1769; DB 6; Length 3868;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2219; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy   1138 CCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCA 1197
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Db   1049 CCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCA 1108

Qy   1198 TGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTG 1257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109 TGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTG 1168

Qy   1258 CAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATG 1317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1169 CAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATG 1228

Qy   1318 GCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACA 1377
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Db   1229 GCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACA 1288

Qy   1378 TCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGA 1437
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Db   1289 TCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGA 1348

Qy   1438 AAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATG 1497
          ||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||
Db   1349 AAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATG 1408

Qy   1498 TGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAAT 1557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1409 TGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAAT 1468

Qy   1558 ACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGA 1617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1469 ACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGA 1528

Qy   1618 GCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACT 1677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1529 GCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACT 1588

Qy   1678 ATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAA 1737
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Db   1589 ATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAA 1648

Qy   1738 GAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCA 1797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1649 GAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCA 1708

Qy   1798 AGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAG 1857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1709 AGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAG 1768

Qy   1858 AGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCT 1917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1769 AGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCT 1828

Qy   1918 GCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCA 1977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1829 GCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCA 1888

Qy   1978 GTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCA 2037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1889 GTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCA 1948

Qy   2038 TGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGT 2097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1949 TGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGT 2008

Qy   2098 ACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCT 2157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 ACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCT 2068

Qy   2158 CTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCA 2217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2069 CTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCA 2128

Qy   2218 GCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGC 2277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2129 GCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGC 2188

Qy   2278 ACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGC 2337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2189 ACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGC 2248

Qy   2338 TCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGA 2397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2249 TCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGA 2308

Qy   2398 ACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTG 2457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2309 ACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTG 2368

Qy   2458 CCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGG 2517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2369 CCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGG 2428
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Qy   2518 AGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAG 2577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2429 AGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAG 2488

Qy   2578 TGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCA 2637
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   2489 TGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCA 2548

Qy   2638 GCTACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACT 2697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2549 GCTACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACT 2608

Qy   2698 CCCCGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCA 2757
            || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2609 TCCTGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCA 2668

Qy   2758 CAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGT 2817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2669 CAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGT 2728

Qy   2818 GGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGG 2877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2729 GGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGG 2788

Qy   2878 TGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCA 2937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2789 TGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCA 2848

Qy   2938 GCTCCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACC 2997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2849 GCTCCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACC 2908

Qy   2998 ACACCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCC 3057
          ||||| |||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   2909 ACACCCGAGATGGCCAGGGTCCCCTGCACCACGGCGTCTGCAGCACATGGCTCAACAGCC 2968

Qy   3058 TGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCG 3117
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   2969 TGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGGCTTCCACCTCCCCG 3028

Qy   3118 AGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCA 3177
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   3029 AGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCA 3088

Qy   3178 GTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGA 3237
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Db   3089 GTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGA 3148

Qy   3238 CCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGG 3297
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Db   3149 CCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGG 3208

Qy   3298 AGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCA 3357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3209 AGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCA 3268

Qy   3358 AGCCCAAG 3365
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Db   3269 AGCCCAAG 3276
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RESULT 15
US-09-724-676A-37687
; Sequence 37687, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 37687
; LENGTH: 3868
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-37687

Query Match 42.7%; Score 1769; DB 6; Length 3868;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2219; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy    1138 CCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCA 1197
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Db    1049 CCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCA 1108

Qy    1198 TGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTG 1257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1109 TGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTG 1168

Qy    1258 CAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATG 1317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1169 CAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATG 1228

Qy    1318 GCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACA 1377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1229 GCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACA 1288

Qy    1378 TCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGA 1437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1289 TCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGA 1348

Qy    1438 AAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATG 1497
           |||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||
Db    1349 AAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATG 1408

Qy    1498 TGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAAT 1557
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Db    1409 TGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAAT 1468

Qy    1558 ACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGA 1617
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Db    1469 ACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGA 1528

Qy    1618 GCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACT 1677
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Qy    1678 ATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAA 1737
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Db    1589 ATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAA 1648

Qy    1738 GAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCA 1797
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Db    1649 GAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCA 1708

Qy    1798 AGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAG 1857
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Db    1709 AGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAG 1768

Qy    1858 AGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCT 1917
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Db    1769 AGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCT 1828

Qy    1918 GCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCA 1977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1829 GCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCA 1888

Qy    1978 GTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCA 2037
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Db    1889 GTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCA 1948

Qy    2038 TGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGT 2097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1949 TGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGT 2008

Qy    2098 ACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCT 2157
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Db    2009 ACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCT 2068

Qy    2158 CTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCA 2217
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Db    2069 CTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCA 2128

Qy    2218 GCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGC 2277
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Db    2129 GCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGC 2188

Qy    2278 ACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGC 2337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2189 ACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGC 2248

Qy    2338 TCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGA 2397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2249 TCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGA 2308

Qy    2398 ACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTG 2457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2309 ACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTG 2368

Qy    2458 CCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGG 2517
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2369 CCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGG 2428

Qy    2518 AGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAG 2577
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Db    2429 AGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAG 2488

Qy    2578 TGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCA 2637
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    2489 TGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCA 2548

Qy    2638 GCTACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACT 2697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2549 GCTACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACT 2608

Qy    2698 CCCCGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCA 2757
           || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2609 TCCTGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCA 2668

Qy    2758 CAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGT 2817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2669 CAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGT 2728

Qy    2818 GGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGG 2877
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Db    2729 GGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGG 2788

Qy    2878 TGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCA 2937
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2789 TGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCA 2848

Qy    2938 GCTCCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACC 2997
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2849 GCTCCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACC 2908

Qy    2998 ACACCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCC 3057
           ||||| |||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    2909 ACACCCGAGATGGCCAGGGTCCCCTGCACCACGGCGTCTGCAGCACATGGCTCAACAGCC 2968

Qy    3058 TGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCG 3117
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    2969 TGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGGCTTCCACCTCCCCG 3028

Qy    3118 AGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCA 3177
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    3029 AGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCA 3088
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Qy    3178 GTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGA 3237
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Db    3089 GTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGA 3148

Qy    3238 CCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGG 3297
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Qy    3298 AGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCA 3357
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3209 AGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCA 3268

Qy    3358 AGCCCAAG 3365
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Db    3269 AGCCCAAG 3276
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Search completed: March 14, 2003, 16:11:33
Job time : 974 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 08:04:33 ; Search time 820 Seconds
(without alignments)
11383.577 Million cell updates/sec

Title: US-09-490-208-3
Perfect score: 4145
Sequence: 1 ctgctttaaaatctctcggc.....aattgcattttactttaatc 4145

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 50

Total number of hits satisfying chosen parameters: 56

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	4145	100.0	4145	15	AAQ66914	Sequence of the cD
	2	4145	100.0	4145	21	AAF20940	Human inducible ni
	3	4145	100.0	4145	21	AAA34818	Human adenosine re
	4	4145	100.0	4145	22	AAH47959	Human inducible ni
	5	4145	100.0	4145	22	AAH47966	Mouse inducible ni
	6	4145	100.0	8222	21	AAF21450	Human inducible ni
	7	4145	100.0	9513	21	AAF20942	Human low adenosin
	8	4145	100.0	9513	21	AAA34820	Human adenosine re
	9	4145	100.0	35384	21	AAF21436	Human enzyme-relat
	10	4043	97.5	4145	17	AAT10115	Nitric oxide synth
	11	3482	84.0	4164	15	AAQ77700	Nitric-oxide-synth
	12	3458	83.4	4070	19	AAT98199	Human inducible ni
	13	3381	81.6	4062	20	AAX08434	Inducible nitric o
	14	3357	81.0	4150	22	AAC67036	Human inducible ni
	15	3327	80.3	3946	22	AAC67035	Human inducible ni
	16	2850	68.8	3462	22	AAH78095	Nucleotide sequenc
	17	1050	25.3	1152	22	AAH78096	Nucleotide sequenc
	18	585	14.1	604	19	AAV35370	Human INOS genomic
	19	585	14.1	604	20	AAZ32098	HiNOS exon 26 nucl
	20	480	11.6	1026	19	AAV35383	Human INOS genomic
	21	480	11.6	1026	20	AAZ32093	HiNOS 3'-untransla
	22	301	7.3	393	23	AAS67653	DNA encoding novel
c	23	255	6.2	450	15	AAQ79427	Human islet induci
	24	185	4.5	497	15	AAQ79426	Human islet induci
c	25	184	4.4	479	22	ABA57910	Human foetal liver
c	26	184	4.4	479	22	AAK05983	Human brain expres
c	27	184	4.4	479	22	AAK31626	Human bone marrow
c	28	184	4.4	479	22	AAI37504	Probe #6190 used t
c	29	184	4.4	479	24	ABS06380	Human genome-deriv
c	30	165	4.0	250	22	ABA70286	Human foetal liver
c	31	165	4.0	250	22	ABA36996	Probe #15462 for g
c	32	165	4.0	250	22	AAK18515	Human brain expres
c	33	165	4.0	250	22	AAK44430	Human bone marrow
c	34	165	4.0	250	22	AAI24864	Probe #14797 for g
c	35	165	4.0	250	22	AAI50424	Probe #19110 used
c	36	165	4.0	250	24	ABS18665	Human genome-deriv
c	37	165	4.0	483	22	ABA57665	Human foetal liver
c	38	165	4.0	483	22	ABA27080	Probe #5546 for ge
c	39	165	4.0	483	22	AAK05722	Human brain expres
c	40	165	4.0	483	22	AAK31343	Human bone marrow
c	41	165	4.0	483	22	AAI15640	Probe #5573 for ge
c	42	165	4.0	483	22	AAI37237	Probe #5923 used t
c	43	165	4.0	483	24	ABS06095	Human genome-deriv
	44	133	3.2	1291	21	AAF20939	Human inducible ni
	45	133	3.2	1291	21	AAA34817	Human adenosine re
	46	133	3.2	1291	24	ABK83638	Human cDNA differe
	47	133	3.2	3117	21	AAF21449	Human inducible ni
	48	110	2.7	1407	24	AAK98736	Polynucleotide of
c	49	92	2.2	92	22	ABA70520	Human foetal liver
c	50	92	2.2	92	22	AAK18765	Human brain expres
c	51	92	2.2	92	22	AAK44701	Human bone marrow
c	52	92	2.2	92	22	AAI50680	Probe #19366 used
c	53	92	2.2	92	24	ABS18938	Human genome-deriv
	54	60	1.4	60	24	ABN59309	Human spliced tran
	55	60	1.4	60	24	ABN59480	Human spliced tran
	56	52	1.3	60	24	ABN35721	Human spliced tran

ALIGNMENTS

RESULT 1
AAQ66914
ID AAQ66914 standard; cDNA; 4145 BP.
XX
AC AAQ66914;
XX
DT 28-DEC-1994 (first entry)
XX
DE Sequence of the cDNA clone for human hepatocyte inducible nitric
DE oxide synthase.
XX
KW Nitric oxide synthase; hepatocyte; hypotensive shock; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 207..3668
FT /*tag= a
XX
PN WO9412645-A.
XX

PD 09-JUN-1994.
XX
PF 23-NOV-1993; 93WO-US11401.
XX
PR 25-NOV-1992; 92US-0981344.
XX
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Billiar TR, Geller DA, Nussler AK, Simmons RL;
XX
DR WPI; 1994-200273/24.
DR P-PSDB; AAR55764.
XX
PT cDNA clone encoding human inducible nitric oxide synthase - used
PT to prevent the hypotensive shock seen with sepsis.
XX
PS Claim 23; Fig 1; 53pp; English.
XX
CC AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA
CC clone pHINOS from lambda Zap II cDNA library. The original source
CC was induced human hepatocyte RNA. HINOS cDNA plasmid is pref.
CC transformed in E. coli SOLR (ATCC 69126). The inventors claim a
CC clone with the cDNA sequence in AAQ66914 and a cDNA clone which
CC encodes AAR55764. The cloning and expression of a human tissue nitric
CC oxide synthase cDNA provides a source of the enzyme for therapeutic
CC purposes, for example to prevent the hypotensive shock seen with
CC sepsis.
XX
SQ Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 other;

Query Match 100.0%; Score 4145; DB 15; Length 4145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
Db     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
Db     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
Db     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
Db     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
Db     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
Db     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
Db     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
Db     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
Db     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
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Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
Db     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
Db     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
Db     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
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Qy    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
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Qy    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
Db    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
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Qy    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
Db    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
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Qy    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Db    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Db    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Db    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
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Qy    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Db    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Db    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
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Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
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Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
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Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
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Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
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Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
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Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
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Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
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Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
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Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
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Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
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Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
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Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
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RESULT 2
AAF20940
ID AAF20940 standard; DNA; 4145 BP.
XX
AC AAF20940;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human inducible nitric oxide synthase polynucleotide fragment #2507.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 254-255; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 other;

Query Match 100.0%; Score 4145; DB 21; Length 4145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
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Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
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Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
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RESULT 3
AAA34818
ID AAA34818 standard; DNA; 4145 BP.
XX
AC AAA34818;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2507.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 664-665; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,

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CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of
CC   the ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680
CC   (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC   invention. N.B. Sequences given in the disclosure of the present
CC   invention do not match up with their corresponding SEQ ID NO: sequences
CC   given in the sequence listing.
XX
SQ   Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 other;

  Query Match             100.0%;  Score 4145;  DB 21;  Length 4145;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy    1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy    1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy    1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy    1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
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Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145


RESULT 4
AAH47959
ID   AAH47959 standard; cDNA; 4145 BP.
XX
AC   AAH47959;
XX
DT   02-OCT-2001  (first entry)
XX
DE   Human inducible nitric oxide synthase encoding cDNA 1.
XX
KW   Antisense oligonucleotide; inducible nitric oxide synthase;
KW   modulate expression; immunomodulator; antidiabetic; cardiovascular;
KW   cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
KW   2'-O-methoxyethyl; phosphorothioate; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             207..3668
FT                   /*tag=  a
FT                   /product= "inducible nitric oxide synthase"
XX
PN   WO200152902-A1.
XX
PD   26-JUL-2001.
XX
PF   15-JAN-2001; 2001WO-US01381.
XX
PR   24-JAN-2000; 2000US-0490208.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Dean NM,  Cowsert LM;
XX
DR   WPI; 2001-465340/50.
DR   P-PSDB; AAG64497.
XX
PT   New antisense oligonucleotides for modulating the expression of
PT   inducible nitric oxide synthase in cells or tissues, particularly
PT   useful for treating e.g. immunological, cardiovascular or neurological
PT   disorders, or ischaemia  -
XX
PS   Example 13; Page 92-97; 144pp; English.
XX
CC   The invention relates to antisense compounds, especially
CC   oligonucleotides, which are targeted to a nucleic acid encoding inducible
CC   nitric oxide synthase and which specifically hybridise to and modulate
CC   expression of inducible nitric oxide synthase. The antisense compounds
CC   have immunomodulator, antidiabetic, cardiovascular, cardiant,
CC   neuroprotective, disorder and vasotropic activity. The antisense
CC   oligonucleotides are useful for inhibiting the expression of inducible
CC   nitric oxide synthase in cells or tissues. In particular, the antisense
CC   oligonucleotides are useful for treating diseases or disorders associated
CC   with inducible nitric oxide synthase, e.g. diabetes, immunological
CC   disorder, cardiovascular disorder, neurological disorder or
CC   ischaemia/reperfusion injury. The antisense oligonucleotides are also
CC   useful for research and diagnostics. The present sequence is that of
CC   human inducible nitric oxide synthase (GenBank accession number L09210).
XX
SQ   Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 other;

  Query Match             100.0%;  Score 4145;  DB 22;  Length 4145;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
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Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy    3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy    3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy    3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy    3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy    3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy    3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy    3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy    3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy    3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy    3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy    3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy    3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy    4141 TAATC 4145
           |||||
Db    4141 TAATC 4145


RESULT 5
AAH47966
ID   AAH47966 standard; cDNA; 4145 BP.
XX
AC   AAH47966;
XX
DT   02-OCT-2001  (first entry)
XX
DE   Mouse inducible nitric oxide synthase encoding cDNA 1.
XX
KW   Antisense oligonucleotide; inducible nitric oxide synthase;
KW   modulate expression; immunomodulator; antidiabetic; cardiovascular;
KW   cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
KW   2'-O-methoxyethyl; phosphorothioate; mouse; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             207..3668
FT                   /*tag= a
FT                   /product= "inducible nitric oxide synthase"
XX
PN   WO200152902-A1.
XX
PD   26-JUL-2001.
XX
PF   15-JAN-2001; 2001WO-US01381.
XX
PR   24-JAN-2000; 2000US-0490208.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Dean NM,  Cowsert LM;
XX
DR   WPI; 2001-465340/50.
DR   P-PSDB; AAG64498.
XX
PT   New antisense oligonucleotides for modulating the expression of
PT   inducible nitric oxide synthase in cells or tissues, particularly
PT   useful for treating e.g. immunological, cardiovascular or neurological
PT   disorders, or ischaemia  -
XX
PS   Example 13; Page 98-103; 144pp; English.
XX
CC   The invention relates to antisense compounds, especially
CC   oligonucleotides, which are targeted to a nucleic acid encoding inducible
CC   nitric oxide synthase and which specifically hybridise to and modulate
CC   expression of inducible nitric oxide synthase. The antisense compounds
CC   have immunomodulator, antidiabetic, cardiovascular, cardiant,
CC   neuroprotective, disorder and vasotropic activity. The antisense
CC   oligonucleotides are useful for inhibiting the expression of inducible
CC   nitric oxide synthase in cells or tissues. In particular, the antisense
CC   oligonucleotides are useful for treating diseases or disorders associated
CC   with inducible nitric oxide synthase, e.g. diabetes, immunological
CC   disorder, cardiovascular disorder, neurological disorder or
CC   ischaemia/reperfusion injury. The antisense oligonucleotides are also
CC   useful for research and diagnostics. The present sequence is that of
CC   mouse inducible nitric oxide synthase (Genbank accession number M92649).
XX
SQ   Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 other;

  Query Match             100.0%;  Score 4145;  DB 22;  Length 4145;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
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Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
```

RESULT 6
AAF21450
ID AAF21450 standard; DNA; 8222 BP.
XX
AC AAF21450;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human inducible nitric oxide synthase polynucleotide fragment #3017.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX

PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 252-254; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 8222 BP; 1731 A; 2574 C; 2360 G; 1557 T; 0 other;

Query Match 100.0%; Score 4145; DB 21; Length 8222;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
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Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy    3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy    3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy    3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy    3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy    3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy    3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy    4141 TAATC 4145
          |||||
Db    4141 TAATC 4145
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RESULT 7
AAF20942
ID AAF20942 standard; DNA; 9513 BP.
XX
AC AAF20942;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide #2509.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 737-739; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 9513 BP; 2107 A; 2868 C; 2672 G; 1866 T; 0 other;

Query Match 100.0%; Score 4145; DB 21; Length 9513;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1292 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 1351

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1352 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 1411

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1412 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 1471

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1472 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 1531

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1532 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 1591

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1592 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 1651

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1652 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 1711

Qy   421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1712 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 1771

Qy   481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1772 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 1831

Qy   541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1832 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 1891

Qy   601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1892 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 1951

Qy   661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1952 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 2011

Qy   721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2012 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 2071

Qy   781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2072 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 2131

Qy   841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2132 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 2191

Qy   901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2192 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 2251

Qy   961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2252 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 2311

Qy  1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2312 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 2371

Qy  1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2372 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 2431

Qy  1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2432 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 2491

Qy  1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2492 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 2551

Qy  1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2552 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 2611

Qy  1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2612 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 2671

Qy  1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2672 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 2731

Qy  1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2732 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 2791

Qy  1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2792 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 2851

Qy  1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2852 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 2911

Qy  1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2912 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 2971

Qy  1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2972 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 3031

Qy  1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3032 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 3091

Qy  1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3092 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 3151

Qy  1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3152 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 3211

Qy  1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3212 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 3271

Qy  1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3272 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 3331

Qy  2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3332 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 3391

Qy  2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3392 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 3451

Qy  2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3452 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 3511

Qy  2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3512 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 3571

Qy  2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3572 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 3631

Qy  2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3632 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 3691

Qy  2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3692 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 3751

Qy  2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3752 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 3811

Qy  2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3812 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 3871
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Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3872 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 3931

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3932 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 3991

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3992 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 4051

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4052 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 4111

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4112 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 4171

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4172 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 4231

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4232 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 4291

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4292 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 4351

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4352 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 4411

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4412 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 4471

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4472 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 4531

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4532 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 4591

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4592 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 4651

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4652 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 4711

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4712 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 4771

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4772 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 4831

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4832 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 4891

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4892 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 4951

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4952 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 5011

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5012 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 5071

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5072 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 5131

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5132 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 5191

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5192 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 5251

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5252 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 5311

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5312 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 5371

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5372 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 5431

Qy   4141 TAATC 4145
          |||||
Db   5432 TAATC 5436
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RESULT 8
AAA34820
ID AAA34820 standard; DNA; 9513 BP.
XX
AC AAA34820;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2509.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,

PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 666-669; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
SQ Sequence 9513 BP; 2107 A; 2869 C; 2671 G; 1866 T; 0 other;

Query Match 100.0%; Score 4145; DB 21; Length 9513;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1292 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 1351

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1352 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 1411

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1412 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 1471

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1472 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 1531

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1532 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 1591

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1592 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 1651

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1652 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 1711

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1712 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 1771

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1772 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 1831

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1832 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 1891

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1892 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 1951

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1952 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 2011

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2012 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 2071

Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2072 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 2131

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2132 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 2191

Qy     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2192 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 2251

Qy     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2252 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 2311

Qy    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2312 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 2371

Qy    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2372 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 2431

Qy    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2432 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 2491

Qy    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2492 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 2551

Qy    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2552 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 2611

Qy    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2612 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 2671

Qy    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2672 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 2731

Qy    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2732 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 2791

Qy    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2792 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 2851

Qy    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2852 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 2911

Qy    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
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Db  2912 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 2971
Qy  1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Db  2972 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 3031
Qy  1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Db  3032 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 3091
Qy  1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Db  3092 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 3151
Qy  1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Db  3152 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 3211
Qy  1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Db  3212 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 3271
Qy  1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Db  3272 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 3331
Qy  2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Db  3332 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 3391
Qy  2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Db  3392 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 3451
Qy  2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Db  3452 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 3511
Qy  2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Db  3512 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 3571
Qy  2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Db  3572 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 3631
Qy  2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Db  3632 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 3691
Qy  2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Db  3692 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 3751
Qy  2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Db  3752 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 3811
Qy  2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Db  3812 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 3871
Qy  2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Db  3872 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 3931
Qy  2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Db  3932 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 3991
Qy  2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Db  3992 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 4051
Qy  2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Db  4052 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 4111
Qy  2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Db  4112 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 4171
Qy  2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Db  4172 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 4231
Qy  2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Db  4232 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 4291
Qy  3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Db  4292 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 4351
Qy  3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Db  4352 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 4411
Qy  3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Db  4412 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 4471
Qy  3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Db  4472 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 4531
Qy  3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
Db  4532 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 4591
Qy  3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
Db  4592 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 4651
Qy  3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
Db  4652 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 4711
Qy  3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
Db  4712 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 4771
Qy  3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
Db  4772 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 4831
Qy  3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
Db  4832 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 4891
Qy  3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
Db  4892 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 4951
Qy  3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
Db  4952 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 5011
Qy  3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
Db  5012 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 5071
Qy  3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
Db  5072 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 5131
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Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5132 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 5191

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5192 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 5251

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5252 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 5311

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5312 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 5371

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5372 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 5431

Qy   4141 TAATC 4145
          |||||
Db   5432 TAATC 5436
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RESULT 9
AAF21436
ID AAF21436 standard; DNA; 35384 BP.
XX
AC AAF21436;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human enzyme-related antisense polynucleotide #3003.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure; Page 47-55; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 35384 BP; 7013 A; 10128 C; 10025 G; 7883 T; 335 other;

Query Match 100.0%; Score 4145; DB 21; Length 35384;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27163 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 27222

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27223 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 27282

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27283 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 27342

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27343 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 27402

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27403 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 27462

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27463 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 27522

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27523 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 27582

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27583 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 27642

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27643 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 27702

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27703 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 27762
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Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27763 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 27822

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27823 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 27882

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27883 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 27942

Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27943 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 28002

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28003 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 28062

Qy     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28063 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 28122

Qy     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28123 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 28182

Qy    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28183 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 28242

Qy    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28243 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 28302

Qy    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28303 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 28362

Qy    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28363 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 28422

Qy    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28423 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 28482

Qy    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28483 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 28542

Qy    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28543 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 28602

Qy    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28603 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 28662

Qy    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28663 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 28722

Qy    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28723 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 28782

Qy    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28783 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 28842

Qy    1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28843 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 28902

Qy    1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28903 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 28962

Qy    1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28963 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 29022

Qy    1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29023 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 29082

Qy    1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29083 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 29142

Qy    1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29143 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 29202

Qy    2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29203 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 29262

Qy    2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29263 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 29322

Qy    2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29323 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 29382

Qy    2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29383 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 29442

Qy    2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29443 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 29502

Qy    2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29503 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 29562

Qy    2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29563 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 29622

Qy    2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29623 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 29682

Qy    2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29683 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 29742

Qy    2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29743 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 29802

Qy    2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29803 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 29862

Qy    2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29863 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 29922

Qy    2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  29923 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 29982

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  29983 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 30042

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30043 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 30102

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30103 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 30162

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30163 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 30222

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30223 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 30282

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30283 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 30342

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30343 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 30402

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30403 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 30462

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30463 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 30522

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30523 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 30582

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30583 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 30642

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30643 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 30702

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30703 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 30762

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30763 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 30822

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30823 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 30882

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30883 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 30942

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30943 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 31002

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31003 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 31062

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31063 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 31122

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31123 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 31182

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31183 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 31242

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31243 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 31302

Qy   4141 TAATC 4145
          |||||
Db  31303 TAATC 31307
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RESULT 10
AAT10115
ID AAT10115 standard; cDNA; 4145 BP.
XX
AC AAT10115;
XX
DT 13-MAY-1996 (first entry)
XX
DE Nitric oxide synthase cDNA clone pHINOS.
XX
KW Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy;
KW vascular occlusive disease; cancer; infection; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   207..3668
FT   /*tag= a
XX
PN WO9600006-A1.
XX
PD 04-JAN-1996.
XX
PF 20-JUN-1995; 95WO-US07849.
XX
PR 24-JUN-1994; 94US-0265046.
XX
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Billiar TR, Geller DA, Nussler AK, Simmons RL, Tzeng E;
XX
DR WPI; 1996-068641/07.
DR P-PSDB; AAR88464.
XX
PT Inducible nitric oxide synthase gene - useful in gene therapy to
PT treat, e.g. vascular occlusive disease and cancer
XX
PS Claim 72; Page 53-58; 91pp; English.
XX
CC A cDNA clone (AAT10115), designated pHINOS, codes for the human
CC hepatocyte inducible nitric oxide synthase (iNOS = AAR88464). It was
CC obtd. by isolating mRNA from hepatocytes induced in vitro for iNOS
CC biosynthesis, preparing a cDNA library in a phage lambda Zap II
CC vector, and screening with a cross-species iNOS probe. The cDNA can
CC be used to prepare iNOS for therapeutic use. Alternatively, it is
CC used in gene therapy strategies for treatment of vascular occlusive
CC disease associated with atherosclerosis, vascular bypass and diabetes
CC mellitus, tumor cell growth, and microbial infections.
XX
SQ Sequence 4145 BP; 968 A; 1205 C; 1124 G; 848 T; 0 other;

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Query Match             97.5%;  Score 4043;  DB 17;  Length 4145;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 4143;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy    1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy    1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy    1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy    1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CGCTCGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy    1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy    1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy    2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy    2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   2701 CGGACATCACCACACCCCCAACCCAGCTCCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
```

RESULT 11
AAQ77700
ID AAQ77700 standard; cDNA; 4164 BP.
XX
AC AAQ77700;
XX
DT 09-MAY-1995 (first entry)

```
XX
DE   Nitric-oxide-synthase pBSHSINOS clone.
XX
KW   Nitric-oxide-synthase; NO-synthase; NOS; chondrocyte;
KW   interleukin-1-beta; pBSHSINOS; arthritis; hypertension;
KW   septic shock; inflammation; ischemia; dementia; obesity; tumor;
KW   agonist; antagonist; vector; CHO; Chinese hamster ovary;
KW   cell culture; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             226..3687
FT                   /*tag=  a
XX
PN   WO9423038-A.
XX
PD   13-OCT-1994.
XX
PF   25-MAR-1994;    94WO-GB00621.
XX
PR   26-MAR-1993;    93GB-0006386.
XX
PA   (WELL ) WELLCOME FOUND LTD.
XX
PI   Charles IG,  Moncada SE,  Palmer RMJ,  Moncada S;
XX
DR   WPI; 1994-333198/41.
DR   P-PSDB; AAR63206.
XX
PT   New human inducible nitric oxide synthase - useful for
PT   identifying enzyme inhibitors and stimulators, and for diagnosis
PT   and treatment of e.g. viral infections or tumours
XX
PS   Disclosure; Page 25-31; 42pp; English.
XX
CC   Human chondrocytes were incubated with interleukin-1-beta to induce
CC   nitric-oxide-synthase.  cDNA was generated and used to construct a
CC   library in lambda ZAPII.  This was screened with a 650 bp fragment of
CC   mouse inducible NO-synthase cDNA to identify the full-length clone
CC   pBSHSINOS.  The insert was transferred to pSVL to give a vector
CC   capable of expressing NO-synthase in CHO cells under control of a
CC   heterologous constitutive promoter.
XX
SQ   Sequence 4164 BP; 974 A; 1210 C; 1127 G; 853 T; 0 other;

  Query Match             84.0%;  Score 3482;  DB 15;  Length 4164;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 4132;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 79

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      80 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 139

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     140 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 199

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     200 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 259

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     260 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 319

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     320 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 379

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     380 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 439

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     440 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 499

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     500 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 559

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     560 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 619

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     620 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 679

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     680 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 739

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     740 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 799

Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     800 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 859

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     860 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 919

Qy     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     920 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 979

Qy     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     980 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1039

Qy    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1040 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1099

Qy    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1100 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1159

Qy    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1160 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1219

Qy    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1220 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1279

Qy    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1280 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1339

Qy    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1340 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1399

Qy    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1400 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1459
```


Qy 1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Db 1460 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATGTGA 1519
Qy 1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Db 1520 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1579
Qy 1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Db 1580 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1639
Qy 1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Db 1640 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1699
Qy 1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Db 1700 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1759
Qy 1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Db 1760 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1819
Qy 1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Db 1820 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1879
Qy 1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Db 1880 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1939
Qy 1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Db 1940 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1999
Qy 1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Db 2000 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2059
Qy 2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Db 2060 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2119
Qy 2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Db 2120 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2179
Qy 2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Db 2180 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2239
Qy 2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Db 2240 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2299
Qy 2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Db 2300 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2359
Qy 2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Db 2360 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2419
Qy 2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Db 2420 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2479
Qy 2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Db 2480 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2539
Qy 2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Db 2540 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGTATCCTGGAGCGAGTGG 2599
Qy 2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Db 2600 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCT 2659
Qy 2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Db 2660 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTTCC 2719
Qy 2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Db 2720 TGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2779
Qy 2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Db 2780 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2839
Qy 2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Db 2840 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2899
Qy 2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Db 2900 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2959
Qy 2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Db 2960 CCTCCCGGGATCACACGCCCACAGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3019
Qy 3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Db 3020 CCCGAGATGGCCAGGGTCCCCTGCACCACGGCGTCTGCAGCACATGGCTCAACAGCCTGA 3079
Qy 3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Db 3080 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGGCTTCCACCTCCCCGAGG 3139
Qy 3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Db 3140 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCAGTT 3199
Qy 3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Db 3200 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3259
Qy 3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
Db 3260 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3319
Qy 3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
Db 3320 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3379
Qy 3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
Db 3380 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3439
Qy 3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
Db 3440 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3499
Qy 3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
Db 3500 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3559
Qy 3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
Db 3560 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTTGGTGCTGTAT 3619
Qy 3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

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Db   3620 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3679

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3680 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3739

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3740 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3799

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3800 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3859

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3860 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3919

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   3920 AGACAAAATCTTAAATGCCAGGCCTGGCAAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3979

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3980 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4039

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4040 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4099

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4100 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4159

Qy   4141 TAATC 4145
          |||||
Db   4160 TAATC 4164
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RESULT 12
AAT98199
ID   AAT98199 standard; cDNA; 4070 BP.
XX
AC   AAT98199;
XX
DT   11-MAY-1998  (first entry)
XX
DE   Human inducible nitric oxide synthetase cDNA.
XX
KW   Nitric oxide synthetase; NOS; iNOS; HPiNOS; human;
KW   erectile dysfunction; impotence; gene therapy; corpora cavernosa;
KW   relaxant; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             197..3658
FT                   /*tag=  a
XX
PN   WO9742965-A1.
XX
PD   20-NOV-1997.
XX
PF   09-MAY-1997;   97WO-US07643.
XX
PR   10-MAY-1996;   96US-0017373.
XX
PA   (GONZ/) GONZALEZ-CADAVID N F.
PA   (RAJF/) RAJFER J.
XX
PI   Gonzalez-Cadavid NF,  Rajfer J;
XX
DR   WPI; 1998-008577/01.
DR   P-PSDB; AAW36113.
XX
PT   Treatment of erectile dysfunction - by introducing an agent into
PT   penile tissue, particularly for inducing cavernosal smooth muscle
PT   relaxation or increasing NOS levels
XX
PS   Claim 14; Page 35-38; 53pp; English.
XX
CC   This cDNA sequence includes a coding region for human penis
CC   inducible nitric oxide synthetase (HPiNOS) (see AAW36113).  It was
CC   isolated by reverse transcription of mRNA from human penile smooth
CC   muscle cells with iNOS antisense primers, combined with PCR
CC   amplification of the resulting cDNA fragments.  The invention is
CC   directed to a method of treating erectile dysfunction in a
CC   patient by providing an agent capable of treating erectile
CC   dysfunction, and introducing an effective amount of the agent into
CC   the penile tissue of the patient.  Preferably, the agent induces
CC   cavernosal smooth muscle relaxation, and/or produces an increase
CC   in the level of NOS in tissue.  Preferably, the NOS is iNOS, and
CC   the agent is introduced into the corpora cavernosa of the penis.
CC   The agent is preferably an NOS inducer, an NOS protein such as
CC   HPiNOS, a cDNA encoding an NOS such as HPiNOS, or cDNA-transformed
CC   penile cells, especially corpora cavernosa cells.
XX
SQ   Sequence 4070 BP; 947 A; 1197 C; 1112 G; 814 T; 0 other;
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  Query Match             83.4%;  Score 3458;  DB 19;  Length 4070;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 4058;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy     11 ATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCGAAGTTCTCAA 70
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCGAAGTTCTCAA 60

Qy     71 GGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGCAGCCAGCTGC 130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGCAGCCAGCTGC 120

Qy    131 AAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAAGTGACCTGCT 190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAAGTGACCTGCT 180

Qy    191 TTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCA 250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCA 240

Qy    251 GTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCCCCTGTGCCAC 310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCCCCTGTGCCAC 300

Qy    311 CTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGA 370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGA 360

Qy    371 GTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGA 430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGA 420

Qy    431 TGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGAC 490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGAC 480

Qy    491 TTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTG 550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTG 540

Qy    551 CCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCC 610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCC 600

Qy    611 TCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCTTCAA 670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCTTCAA 660
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Qy    671 AGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAAC 730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAAC 720

Qy    731 AACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCG 790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCG 780

Qy    791 CAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCG 850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCG 840

Qy    851 CAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCAC 910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCAC 900

Qy    911 CAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCA 970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCA 960

Qy    971 CGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGG 1030
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGG 1020

Qy   1031 CAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCGACCTGGGCTG 1090
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCGACCTGGGCTG 1080

Qy   1091 GAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGA 1150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGA 1140

Qy   1151 CCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAA 1210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAA 1200

Qy   1211 ATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACAT 1270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACAT 1260

Qy   1271 GCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGG 1330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGG 1320

Qy   1331 CACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCCTGGAGGAAGT 1390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCCTGGAGGAAGT 1380

Qy   1391 GGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGT 1450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGT 1440

Qy   1451 CGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGACCATCATGGA 1510
          |||||||||||||| ||||||| |||||||| ||||||||||||||||||||||||||||||
Db   1441 CGTTGAGATCAACACTGCTGTGCTCCATAGTTCTCAGAAGCAGAATGTGACCATCATGGA 1500

Qy   1511 CCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGG 1570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGG 1560

Qy   1571 GGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGT 1630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGT 1620

Qy   1631 GTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGC 1690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGC 1680

Qy   1691 CTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAGAGATTCCATT 1750
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAGAGATTCCATT 1740
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Qy   1751 GAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGACAATGGCGTC 1810
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGACAATGGCGTC 1800

Qy   1811 CCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGGCGCTGGCCTG 1870
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGGCGCTGGCCTG 1860

Qy   1871 GGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCATGGATAAGTA 1930
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 GGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCATGGATAAGTA 1920

Qy   1931 CAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTACGTTTGGCAA 1990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTACGTTTGGCAA 1980

Qy   1991 TGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGCTGAAAGAGCT 2050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGCTGAAAGAGCT 2040

Qy   2051 CAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACCCTCGGTTCTG 2110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACCCTCGGTTCTG 2100

Qy   2111 CGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTCAGCTCACCCC 2170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTCAGCTCACCCC 2160

Qy   2171 GATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCTGGGCCGTGCA 2230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCTGGGCCGTGCA 2220

Qy   2231 AACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACATTCAGATCCC 2290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACATTCAGATCCC 2280

Qy   2291 CAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCGTGCAGGACTC 2350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCGTGCAGGACTC 2340

Qy   2351 ACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCAT 2410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 ACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCAT 2400

Qy   2411 GAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGT 2470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGT 2460

Qy   2471 GGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGCACCTTGGGGT 2530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGCACCTTGGGGT 2520

Qy   2531 TTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGGTGGATGGCCC 2590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGGTGGATGGCCC 2580

Qy   2591 CACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCTACTGGGTCAG 2650
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   2581 CACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCTACTGGGTCAG 2640

Qy   2651 TGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCCCGGACATCAC 2710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCCCGGACATCAC 2700

Qy   2711 CACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAGAAGAGCCTGA 2770
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAGAAGAGCCTGA 2760

Qy   2771 GAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGAAGTTCACCAA 2830
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGAAGTTCACCAA 2820

Qy   2831 CAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGTCTGCTGGCTT 2890
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Db   2821 CAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGTCTGCTGGCTT 2880

Qy   2891 CCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCTCCTCCCGGGA 2950
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCTCCTCCCGGGA 2940

Qy   2951 TCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACACCGGAGATGG 3010
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   2941 TCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACACCCGAGATGG 3000

Qy   3011 CCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGAAGCCCCAAGA 3070
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   3001 CCAGGGTCCCCTGCACCACGGCGTCTGCAGCACATGGCTCAACAGCCTGAAGCCCCAAGA 3060

Qy   3071 CCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGGATCCCTCCCA 3130
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   3061 CCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGGCTTCCACCTCCCCGAGGATCCCTCCCA 3120

Qy   3131 TCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTTTCTGGCAGCA 3190
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   3121 TCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCAGTTTCTGGCAGCA 3180

Qy   3191 ACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCTTGGTGTTTGG 3250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 ACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCTTGGTGTTTGG 3240

Qy   3251 GTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGATGGCCCAGAA 3310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGATGGCCCAGAA 3300

Qy   3311 GGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGCCCAAGGTCTA 3370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGCCCAAGGTCTA 3360

Qy   3371 TGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGCTCCACAAGGA 3430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGCTCCACAAGGA 3420

Qy   3431 GCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGGCCCACACCCT 3490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 GCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGGCCCACACCCT 3480

Qy   3491 GAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGGACTATTTCTT 3550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGGACTATTTCTT 3540

Qy   3551 TCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTATTTCCTTACGA 3610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTATTTCCTTACGA 3600

Qy   3611 GGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAGCGCTCTGAGG 3670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAGCGCTCTGAGG 3660

Qy   3671 GCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATT 3730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATT 3720

Qy   3731 ATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTT 3790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 ATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTT 3780

Qy   3791 ATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCT 3850
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 ATTTCCTCAACTTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCT 3840

Qy   3851 GGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATC 3910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATC 3900

Qy   3911 TTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTC 3970
          || |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||

Db   3901 TTTAATGCCAGGCCCGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTC 3960

Qy   3971 AAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTA 4030
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 AATTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTA 4020

Qy   4031 TTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4070
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RESULT 13
AAX08434
ID AAX08434 standard; DNA; 4062 BP.
XX
AC AAX08434;
XX
DT 28-JUN-1999 (first entry)
XX
DE Inducible nitric oxide synthase gene.
XX
KW Manganese containing superoxide dismutase; MnSOD; IDDM;
KW diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell;
KW fatty acids; lipotoxic; cytotoxic; cytokine; osteoporosis;
KW inflammatory disease; autoimmune disease; neurodegenerative disease;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 106..3567
FT /*tag= a
FT /product= "Nitric oxide synthase"
XX
PN WO9906059-A2.
XX
PD 11-FEB-1999.
XX
PF 30-JUL-1998; 98WO-US15781.
XX
PR 03-MAR-1998; 98US-0055092.
PR 30-JUL-1997; 97US-0055092.
XX
PA (BETA-) BETAGENE INC.
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Clark SA, Hohmeier H, Koyama K, Lee Y, Newgard CB;
PI Ohneda M, Shimabukurom, Thigpen A, Unger RH;
XX
DR WPI; 1999-153448/13.
DR P-PSDB; AAW96322.
XX
PT Protection of mammalian cells against immunotoxicity or lipotoxicity
PT - used for treating, e.g. diabetes, obesity, wasting syndromes,
PT osteoporosis, inflammatory diseases, autoimmune diseases or
PT neurodegenerative diseases
XX
PS Disclosure; Page 244-247; 253pp; English.
XX
CC Inhibition of cytokine mediated immunotoxicity of cells can be
CC achieved by blocking free radical production or the accumulation of
CC free radicals in that cell. Treatment of insulin dependent diabetes
CC mellitus (IDDM) can be achieved by by blocking nitric oxide (NO)
CC production in a pancreatic beta cell and by providing a composition
CC comprising an agent that reduces levels of fatty acids in the cells
CC and protects beta-cells of the subject against lipid-mediated cell
CC death. Cells can also be protected against nitric oxide mediated
CC cytotoxicity by introducing into the cell an antioxidising agent.
CC The methods can be used for protecting cells against immunotoxicity
CC mediated by, e. g. 1L-1 beta, 1L-1 alpha, gamma IFN, TNF alpha, TNF
CC beta, IL-8, IL-2, IL-6, IL-2, IL-3, IL-5, IL-7, IL-9, IL-14, IL-17,
CC granulocyte-macrophage colony stimulating factor or monocyte
CC chemoattractant protein-1. The methods can be used for the treatment

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CC   of e.g.  insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity,
CC   wasting syndromes, short stature, osteoporosis, inflammatory
CC   diseases, autoimmune diseases, or neurodegenerative diseases.
XX
SQ   Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 other;

  Query Match             81.6%;  Score 3381;  DB 20;  Length 4062;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 4031;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy    102 TACCCCGGGGAGGCAGTGCAGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAA 161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TACCCCGGGGAGGCAGTGCAGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAA 60

Qy    162 ATCCAGATAAGTGACATAAGTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGG 221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATCCAGATAAGTGACATAAGTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGG 120

Qy    222 AAATTTCTGTTCAAGACCAAATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAAC 281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAATTTCTGTTCAAGACCAAATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAAC 180

Qy    282 AACAATGTGGAGAAAGCCCCCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAG 341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AACAATGTGGAGAAAGCCCCCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAG 240

Qy    342 TATCACAACCTCAGCAAGCAGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAG 401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TATCACAACCTCAGCAAGCAGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAG 300

Qy    402 AAGTCTCCAGAATCTCTGGTCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTG 461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AAGTCTCCAGAATCTCTGGTCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTG 360

Qy    462 AGGATCAAAAACTGGGGCAGCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAA 521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGGATCAAAAACTGGGGCAGCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAA 420

Qy    522 GGGATTTTAACTTGCAGGTCCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTG 581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGGATTTTAACTTGCAGGTCCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTG 480

Qy    582 ACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAA 641
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAA 540

Qy    642 TTTGTCAACCAATATTACGGCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGG 701
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TTTGTCAACCAATATTACGGCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGG 600

Qy    702 GTGGAAGCGGTAACAAAGGAGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAG 761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTGGAAGCGGTAACAAAGGAGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAG 660

Qy    762 CTCATCTTCGCCACCAAGCAGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAG 821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCATCTTCGCCACCAAGCAGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAG 720

Qy    822 TGGTCCAACCTGCAGGTCTTCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAA 881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TGGTCCAACCTGCAGGTCTTCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAA 780

Qy    882 CACATCTGCAGACACGTGCGTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACC 941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CACATCTGCAGACACGTGCGTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACC 840

Qy    942 GTGTTCCCCCAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATC 1001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GTGTTCCCCCAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATC 900

Qy   1002 CGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAA 1061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAA 960

Qy   1062 TTCACTCAGCTGTGCATCGACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTC 1121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TTCACTCAGCTGTGCATCGACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTC 1020

Qy   1122 CCCCTGGTCCTGCAGGCCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTT 1181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CCCCTGGTCCTGCAGGCCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTT 1080

Qy   1182 GTGCTTGAGGTGGCCATGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAG 1241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GTGCTTGAGGTGGCCATGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAG 1140

Qy   1242 TGGTACGCCCTGCCTGCAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCA 1301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TGGTACGCCCTGCCTGCAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCA 1200

Qy   1302 GGGTGCCCCCTTCAATGGCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGAC 1361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GGGTGCCCCTTCAATGGCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGAC 1260

Qy   1362 GTCCAGCGCTACAACATCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAG 1421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTCCAGCGCTACAACATCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAG 1320

Qy   1422 CTGGCCTCGCTCTGGAAAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGT 1481
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    1321 CTGGCCTCGCTCTGGAAAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGT 1380

Qy   1482 TTTCAGAAGCAGAATGTGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAG 1541
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TTCCAGAAGCAGAATGTGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAG 1440

Qy   1542 TACATGCAGAATGAATACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTC 1601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TACATGCAGAATGAATACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTC 1500

Qy   1602 CCTCCCATGTCTGGGAGCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTG 1661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CCTCCCATGTCTGGGAGCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTG 1560

Qy   1662 TCCCCTTTCTACTACTATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAG 1721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 TCCCCTTTCTACTACTATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAG 1620

Qy   1722 CGGAGACCCAAGAGAAGAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCC 1781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 CGGAGACCCAAGAGAAGAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCC 1680

Qy   1782 TGTATGCTGATGCGCAAGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACA 1841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 TGTATGCTGATGCGCAAGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACA 1740

Qy   1842 GAGACAGGAAAATCAGAGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTC 1901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GAGACAGGAAAATCAGAGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTC 1800

Qy   1902 AACCCCAAGGTTGTCTGCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTG 1961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AACCCCAAGGTTGTCTGCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTG 1860

Qy   1962 CTGTTGGTGGTGACCAGTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTG 2021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CTGTTGGTGGTGACCAGTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTG 1920

Qy   2022 AAGAAATCGCTCTTCATGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGC 2081
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 AAGAAATTGCTCTTCATGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGC 1980

Qy   2082 CTCGGCTCCAGCATGTACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTG 2141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CTCGGCTCCAGCATGTACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTG 2040
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Qy   2142 TCCCACCTGGGGGCCTCTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAG 2201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TCCCACCTGGGGGCCTCTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAG 2100

Qy   2202 GAGGACGCCTTCCGCAGCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGAT 2261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GAGGACGCCTTCCGCAGCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGAT 2160

Qy   2262 GTCCGAGGCAAACAGCACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGAC 2321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GTCCGAGGCAAACAGCACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGAC 2220

Qy   2322 CCGCACCACTACAGGCTCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGC 2381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CCGCACCACTACAGGCTCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGC 2280

Qy   2382 AGCATGCATGCCAAGAACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGT 2441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AGCATGCATGCCAAGAACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGT 2340

Qy   2442 CCGACATCCAGCCGTGCCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTG 2501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCGACATCCAGCCGTGCCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTG 2400

Qy   2502 AACTACCTGCCGGGGGGAGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAA 2561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 AACTACCTGCCGGGGGAGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAA 2460

Qy   2562 GGCATCCTGGAGCGAGTGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGAC 2621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   2461 GGCATCCTGGAGCGAGTGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCC 2520

Qy   2622 CTGGATGAGAGTGGCAGCTACTGGGTCAGTGACAAGAGGCTGCCCCCCCTGCTCACTCAGC 2681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 CTGGATGAGAGTGGCAGCTACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGC 2580

Qy   2682 CAGGCCCTCACCTACTCCCCGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAG 2741
          |||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db   2581 CAGGCCCTCACCTACTTCCTGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAG 2640

Qy   2742 CTGGCCCAGGTGGCCACAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCC 2801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 CTGGCCCAGGTGGCCACAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCC 2700

Qy   2802 TCAGAGTACAGCAAGTGGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAG 2861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TCAGAGTACAGCAAGTGGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAG 2760

Qy   2862 TTCCCGTCCCTGCGGGTGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCC 2921
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TTCCCGTCCCTGCGGGTGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCC 2820

Qy   2922 AGGTTCTACTCCATCAGCTCCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTG 2981
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   2821 AGGTTCTACTCCATCAGCTCCTCCCGGGATCACACGCCCACAGAGATCCACCTGACTGTG 2880

Qy   2982 GCCGTGGTCACCTACCACACCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGC 3041
          |||||||||||||||||||| |||||||||||||||||||||||| |||||||||||||||
Db   2881 GCCGTGGTCACCTACCACACCCGAGATGGCCAGGGTCCCCTGCACCACGGCGTCTGCAGC 2940

Qy   3042 ACATGGCTCAACAGCCTGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGC 3101
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 ACATGGCTCAACAGCCTGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGC 3000

Qy   3102 GCCTTCCACCTCCCCGAGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGC 3161
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GGCTTCCACCTCCCCGAGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGC 3060

Qy   3162 ATCGTGCCCTTCCGCAGTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTG 3221
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 ATCGCGCCCTTCCGCAGTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTG 3120

Qy   3222 CGGGGAGGCCGCATGACCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTAC 3281
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Db   3121 CGGGGAGGCCGCATGACCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTAC 3180

Qy   3282 CAGGAGGAGATGCTGGAGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTAT 3341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CAGGAGGAGATGCTGGAGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTAT 3240

Qy   3342 TCCCGCCTGCCTGGCAAGCCCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCC 3401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TCCCGCCTGCCTGGCAAGCCCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCC 3300

Qy   3402 AGCGAGGTGCTCCGTGTGCTCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTG 3461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 AGCGAGGTGCTCCGTGTGCTCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTG 3360

Qy   3462 CGCATGGCCCGGGACGTGGCCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTG 3521
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Db   3361 CGCATGGCCCGGGACGTGGCCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTG 3420

Qy   3522 AATGAGGAGCAGGTCGAGGACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAA 3581
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Db   3421 AATGAGGAGCAGGTCGAGGACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAA 3480

Qy   3582 GATATCTTCGGTGCTGTATTTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCC 3641
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GATATCTTTGGTGCTGTATTTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCC 3540

Qy   3642 AGCAGCCTGGAGATGTCAGCGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACA 3701
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Db   3541 AGCAGCCTGGAGATGTCAGCGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACA 3600

Qy   3702 GAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAG 3761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAG 3660

Qy   3762 GAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCT 3821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCT 3720

Qy   3822 TTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGG 3881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGG 3780

Qy   3882 GGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAG 3941
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   3781 GGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGCCTGGCAAGTGGGTGAAAG 3840

Qy   3942 ATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCAC 4001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCAC 3900

Qy   4002 TGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACC 4061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACC 3960

Qy   4062 CAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTA 4121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTA 4020

Qy   4122 CATGAATTGCATTTTACTTTAATC 4145
          |||||||||||||||||||||||
Db   4021 CATGAATTGCATTTTACTTTAATC 4044
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RESULT 14
AAC67036
ID AAC67036 standard; DNA; 4150 BP.
XX
AC AAC67036;
XX
DT 03-APR-2001 (first entry)
XX
DE Human inducible nitric oxide synthase coding sequence #2.

XX
KW Human; influenza virus; antisense; inducible nitric oxide synthase;
KW iNOS; ds.
XX
OS Homo sapiens.
XX
PN WO200078946-A2.
XX
PD 28-DEC-2000.
XX
PF 19-JUN-2000; 2000WO-US16810.
XX
PR 17-JUN-1999; 99US-0139479.
XX
PA (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.
XX
PI Keller ET, Gravenstein S, Hall DM;
XX
DR WPI; 2001-102720/11.
XX
PT Treating viral influenza with antisense oligonucleotides that hybridize
PT with inducible nitride oxide synthase mRNA and inhibit synthesis of the
PT enzyme, reducing the production of nitric oxide in lungs -
XX
PS Disclosure; Fig 2; 21pp; English.
XX
CC The present invention provides a novel method of treating influenza virus
CC infection by administering an antisense oligonucleotide directed at the
CC human inducible nitric oxide synthase (iNOS) mRNA. This is useful in
CC preventing the symptoms of influenza infection.
XX
SQ Sequence 4150 BP; 968 A; 1211 C; 1125 G; 846 T; 0 other;

Query Match 81.0%; Score 3357; DB 22; Length 4150;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 4107; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     29 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 88

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 148

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    149 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 208

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    209 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 268

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    269 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 328

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    329 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 388

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    389 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 448

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    449 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 508

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    509 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 568

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    569 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 628

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    629 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 688

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    689 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 748

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    749 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 808

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    809 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 868

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
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Db    869 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 928

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    929 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 988

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    989 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCACTATGCTGGCTACCAGA 1048

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1049 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1108

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1168

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1169 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1228

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
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Db   1229 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1288

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
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Db   1289 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1348

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
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Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
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Db   1409 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1468

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   1469 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGTTTTCAGAAGCAGAATGTGA 1528

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
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Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1589 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1648

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
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Db   1649 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1708

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Db   1709 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1768

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Db   1769 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1828

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Db   1829 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCTACAGAGACAGGAAAATCAGAGG 1888

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Db   1889 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1948

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Db   1949 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 2008

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Db   2069 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2128

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Db   2129 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2188

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Db   2189 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2248

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Db   2249 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2308

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Db   2309 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2368

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Db   2369 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2428

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Db   2429 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2488

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Db   2549 ACCTTGGGGTTTGTCCAGGCAACCAGCCGGCCCTGGTCCAAGGTATCCTGGAGCGAGTGG 2608

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Db   2609 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCT 2668

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTTCC 2700

Db   2669 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTTCC 2728

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Db   2729 TGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2788

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Db   2789 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2848

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

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Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Db   2909 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2968

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Db   2969 CCTCCCGGGATCACACGCCCACAGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3028

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Db   3029 CCCGAGATGGCCAGGGTCCCCTGCACCACGGCGTCTGCAGCACATGGCTCAACAGCCTGA 3088

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Db   3149 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCAGTT 3208

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Db   3209 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3268

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Db   3269 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3328

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

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Db   3389 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3448

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Db   3449 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3508

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Db   3509 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3568

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Db   3569 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTTGGTGCTGTAT 3628

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Db   3629 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3688

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Db   3689 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3748

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Db   3749 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3808

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Db   3809 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3868
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Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
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Db   3869 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3928

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Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
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Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTAC 4122
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Db   4109 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTAC 4150
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RESULT 15
AAC67035
ID AAC67035 standard; DNA; 3946 BP.
XX
AC AAC67035;
XX
DT 03-APR-2001 (first entry)
XX
DE Human inducible nitric oxide synthase coding sequence #1.
XX
KW Human; influenza virus; antisense; inducible nitric oxide synthase;
KW iNOS; ds.
XX
OS Homo sapiens.
XX
PN WO200078946-A2.
XX
PD 28-DEC-2000.
XX
PF 19-JUN-2000; 2000WO-US16810.
XX
PR 17-JUN-1999; 99US-0139479.
XX
PA (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.
XX
PI Keller ET, Gravenstein S, Hall DM;
XX
DR WPI; 2001-102720/11.
XX
PT Treating viral influenza with antisense oligonucleotides that hybridize
PT with inducible nitride oxide synthase mRNA and inhibit synthesis of the
PT enzyme, reducing the production of nitric oxide in lungs -
XX
PS Disclosure; Fig 1; 21pp; English.
XX
CC The present invention provides a novel method of treating influenza virus
CC infection by administering an antisense oligonucleotide directed at the
CC human inducible nitric oxide synthase (iNOS) mRNA. This is useful in
CC preventing the symptoms of influenza infection.
XX
SQ Sequence 3946 BP; 918 A; 1149 C; 1073 G; 806 T; 0 other;

Query Match 80.3%; Score 3327; DB 22; Length 3946;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3927; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy    207 ATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCAGTATGCAATGAATGGG 266
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Db      1 ATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCAGTATGCAATGAATGGG 60

Qy    267 GAAAAAGACATCAACAACAATGTGGAGAAAGCCCCCTGTGCCACCTCCAGTCCAGTGACA 326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GAAAAAGACATCAACAACAATGTGGAGAAAGCCCCCTGTGCCACCTCCAGTCCAGTGACA 120

Qy    327 CAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGAGTCCCCGCAGCCCCTC 386
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Db    121 CAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGAGTCCCCGCAGCCCCTC 180

Qy    387 GTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGATGCAACCCCATTGTCC 446
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Db    181 GTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGATGCAACCCCATTGTCC 240

Qy    447 TCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGACTTTCCAAGACACACTT 506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    507 CACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTGCCTGGGGTCCATTATG 566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTGCCTGGGGTCCATTATG 360

Qy    567 ACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTA 626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTA 420

Qy    627 CCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCTTCAAAGAGGCAAAAATAGAG 686
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Qy    687 GAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAACAACAGGAACCTACCAA 746
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Qy    747 CTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCAATGCCCCACGCTGC 806
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Db    541 CTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCAATGCCCCACGCTGC 600

Qy    807 ATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCGCAGCTGTTCCACTGCC 866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCGCAGCTGTTCCACTGCC 660

Qy    867 CGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCACCAACAATGGCAACATC 926
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Db    661 CGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCACCAACAATGGCAACATC 720

Qy    927 AGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGG 986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGG 780

Qy    987 AATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGAC 1046
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Qy   1047 CCTGCCAACGTGGAATTCACTCAGCTGTGCATCGACCTGGGCTGGAAGCCCAAGTACGGC 1106
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Qy   1107 CGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGACCCTGAGCTCTTCGAA 1166
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Qy   1167 ATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAAATACGAGTGGTTTCGG 1226
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Qy   1227 GAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACATGCTGCTTGAGGTGGGC 1286
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Db    1021 GAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACATGCTGCTTGAGGTGGGC 1080

Qy   1287 GGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGGCACAGAGATCGGAGTC 1346
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Db    1081 GGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGGCACAGAGATCGGAGTC 1140

Qy   1347 CGGGACTTCTGTGACGTCCAGCGCTACAACATCCTGGAGGAAGTGGGCAGGAGAATGGGC 1406
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Db   1141 CGGGACTTCTGTGACGTCCAGCGCTACAACATCCTGGAGGAAGTGGGCAGGAGAATGGGC 1200

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Db   1201 CTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGTCGTTGAGATCAACATT 1260

Qy   1467 GCTGTGATCCATAGTTTTCAGAAGCAGAATGTGACCATCATGGACCACCACTCGGCTGCA 1526
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Db   1261 GCTGTGCTCCATAGTTTCCAGAAGCAGAATGTGACCATCATGGACCACCACTCGGCTGCA 1320

Qy   1527 GAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGGGGGCTGCCCGGCAGAC 1586
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Db   1321 GAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGGGGGCTGCCCGGCAGAC 1380

Qy   1587 TGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGTGTTTCACCAGGAGATG 1646
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Qy   1647 CTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGCCTGGAAAACCCATGTC 1706
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Scoring table: OLIGO_NUC
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Searched: 501302 seqs, 350932545 residues

Word size : 50

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Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	248	6.0	256	10	US-09-998-598-1831	Sequence 1831, Ap
c 2	184	4.4	479	10	US-09-864-761-10947	Sequence 10947, A
c 3	174	4.2	174	10	US-09-998-598-1881	Sequence 1881, Ap
c 4	165	4.0	250	10	US-09-864-761-22316	Sequence 22316, A
c 5	165	4.0	483	10	US-09-864-761-5546	Sequence 5546, Ap
c 6	92	2.2	92	10	US-09-864-761-27584	Sequence 27584, A

ALIGNMENTS

RESULT 1
US-09-998-598-1831/c
; Sequence 1831, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 1831
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-1831

Query Match 6.0%; Score 248; DB 10; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.8e-118;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 10947, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

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;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10947
;   LENGTH: 479
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC005697.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.84
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.92
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.99
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.79
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.95
US-09-864-761-10947

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RESULT 3
US-09-998-598-1881/c
; Sequence 1881, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
;  APPLICANT: Stolk, John A.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Chenault, Ruth A.
;  APPLICANT:  Meagher, Madelein Joy
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.561
;  CURRENT APPLICATION NUMBER: US/09/998,598
;  CURRENT FILING DATE:  2001-11-16
;  NUMBER OF SEQ ID NOS: 2606
;  SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 1881
;   LENGTH: 174
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-998-598-1881

  Query Match             4.2%;  Score 174;  DB 10;  Length 174;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-79;
  Matches  174;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 4
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; Sequence 22316, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 22316
;   LENGTH: 250
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC005697.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.9
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.5
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.2
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.3
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.7
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.6
;   OTHER INFORMATION: NT HIT: X85764.1, EVALUE 1.00e-127
;   OTHER INFORMATION: SWISSPROT HIT: O62699, EVALUE 2.00e-26
US-09-864-761-22316

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  Best Local Similarity   100.0%;  Pred. No. 6.6e-75;
  Matches  165;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     250 GGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAACAAC 191

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     190 AGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCAA 131

Qy     794 TGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGT 838
           |||||||||||||||||||||||||||||||||||||||||||||
Db     130 TGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGT 86


RESULT 5
US-09-864-761-5546/c
; Sequence 5546, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5546
;   LENGTH: 483
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC005697.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.9
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.5
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.2
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.3
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.7
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.6
US-09-864-761-5546

  Query Match             4.0%;  Score 165;  DB 10;  Length 483;
  Best Local Similarity   100.0%;  Pred. No. 7e-75;
  Matches  165;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     674 GGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAACAAC 733
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     479 GGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAACAAC 420

Qy     734 AGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCAA 793
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Db     419 AGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCAA 360

Qy     794 TGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGT 838
           |||||||||||||||||||||||||||||||||||||||||||||
Db     359 TGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGT 315


RESULT 6
US-09-864-761-27584/c
; Sequence 27584, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
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;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27584
;   LENGTH: 92
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC005697.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.84
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.92
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.99
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.79
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.95
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;   OTHER INFORMATION: SWISSPROT HIT: P35228, EVALUE 3.00e-13
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US-09-864-761-27584

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Job time : 275 secs
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 50

Total number of hits satisfying chosen parameters: 47

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
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11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	12	289	7.0	355	10	AW449618	AW449618 UI-H-BI3-
	13	269	6.5	541	10	AW391328	AW391328 QV0-ST021
	14	231	5.6	377	10	AW950112	AW950112 EST362077
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c	16	216	5.2	705	10	AW001205	AW001205 wu25h08.x
c	17	214	5.2	555	9	AA583269	AA583269 nn41g02.s
	18	205	4.9	325	9	AA351050	AA351050 EST58635
c	19	198	4.8	260	12	BG099280	BG099280 nad99h08.
c	20	165	4.0	867	17	AQ750612	AQ750612 HS_5573_B
c	21	156	3.8	278	9	AA515493	AA515493 nf65g06.s
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c	23	134	3.2	554	17	AQ498523	AQ498523 HS_5120_B
	24	131	3.2	168	10	BE073577	BE073577 RC5-BT055
	25	131	3.2	168	10	BE073638	BE073638 RC5-BT055
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c	27	121	2.9	366	14	T15817	T15817 IB1935 Infa
c	28	96	2.3	327	14	H67843	H67843 yu67a05.s1
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	30	90	2.2	276	9	AA352011	AA352011 EST59932
c	31	89	2.1	517	17	AQ629240	AQ629240 RPCI-11-4
	32	82	2.0	583	17	AQ525238	AQ525238 HS_5227_B
	33	77	1.9	177	17	AQ634346	AQ634346 RPCI-11-4
c	34	77	1.9	470	17	AQ095690	AQ095690 HS_3017_A
c	35	69	1.7	523	17	AQ800595	AQ800595 HS_5314_B
c	36	68	1.6	833	17	AQ749776	AQ749776 HS_5573_A
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	38	62	1.5	360	14	BQ326829	BQ326829 PM2-CN015
c	39	62	1.5	619	17	AG156646	AG156646 Pan trogl
	40	61	1.5	235	14	H67165	H67165 yu67a05.r1
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c	43	50	1.2	460	9	AI640427	AI640427 tz70g12.x
c	44	50	1.2	519	9	AA432369	AA432369 zw76b04.s
c	45	50	1.2	532	9	AA432381	AA432381 zw76d02.s
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ALIGNMENTS

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DEFINITION wi36f02.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392347 3' similar to gb:X73029 NITRIC OXIDE SYNTHASE, INDUCIBLE (HUMAN);, mRNA sequence.
ACCESSION AI738789
VERSION AI738789.1 GI:5100770
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 721)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

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           www-bio.llnl.gov/bbrp/image/image.html
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           High quality sequence stop: 471.
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                     /clone_lib="NCI_CGAP_Co16"
                     /tissue_type="colon tumor, RER+"
                     /lab_host="DH10B"
                     /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Co10 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1057416-1061255, and 1144584-1145351).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT      179 a    186 c    183 g    172 t      1 others
ORIGIN

  Query Match            12.4%;  Score 513;  DB 9;  Length 721;
  Best Local Similarity  99.7%;  Pred. No. 1.2e-242;
  Matches  613;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy    3591 GGTGCTGTATTTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTG 3650
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     555 GGTGCTGTATTTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTG 496

Qy    3651 GAGATGTCAGCGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAG 3710
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     495 GAGATGTCAGCGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAG 436

Qy    3711 GATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGAT 3770
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Db     435 GATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGAT 376

Qy    3771 ATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGAC 3830
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     375 ATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGAC 316

Qy    3831 CTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCT 3890
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Qy    4011 AACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTT 4070
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Db      75 CCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTG 16

Qy    4131 CATTTTACTTTAATC 4145
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Db      15 CATTTTACTTTAATC 1
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AI953734/c
LOCUS       AI953734                470 bp    mRNA    linear   EST 06-SEP-1999
DEFINITION  wq47g02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2474450 3'
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            mRNA sequence.
ACCESSION   AI953734
VERSION     AI953734.1  GI:5746044
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 470)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .470
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2474450"
                     /clone_lib="NCI_CGAP_GC6"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     1257096-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT      128 a    107 c    121 g    114 t
ORIGIN

  Query Match            10.1%;  Score 417;  DB 9;  Length 470;
  Best Local Similarity  99.8%;  Pred. No. 4.5e-195;
  Matches  467;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    3678 GGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAG 3737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     470 GGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAG 411

Qy    3738 GTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCT 3797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     410 GTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCT 351

Qy    3798 CAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGA 3857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     350 CAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGA 291

Qy    3858 TCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATG 3917
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     290 TCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATG 231

Qy    3918 CCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGAC 3977
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     230 CCAGGCCTGGCAAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGAC 171
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Qy   3978 CACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGC 4037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    170 CACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGC 111

Qy   4038 CTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGT 4097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    110 CTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGT 51

Qy   4098 ATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTTTAATC 4145
          |||||||||||||||||||||||||||||||||||||||||||||||
Db     50 ATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTTTAATC 3
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RESULT 3
AI991263/c

LOCUS	AI991263 453 bp mRNA linear EST 09-MAR-2000
DEFINITION	wu41f10.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522635 3' similar to gb:X73029 NITRIC OXIDE SYNTHASE, INDUCIBLE (HUMAN);, mRNA sequence.
ACCESSION	AI991263
VERSION	AI991263.1 GI:5838168
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 453)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 576 Std Error: 0.00 Seq primer: -40UP from Gibco.

FEATURES Location/Qualifiers

source 1. .453
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2522635"
/clone_lib="Soares_Dieckgraefe_colon_NHCD"
/tissue_type="colonic mucosa from 3 patients with Crohn's disease"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCGTCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Tissue samples provided by Dr. Brian Dieckgraefe (Washington University, dieck@im.wustl.edu); colonic mucosa represents a range of disease involvement from moderate to severe Crohn's disease; samples include both perforating (fistulas) and non-perforating samples. Library constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 125 a 101 c 119 g 108 t
ORIGIN

Query Match 9.7%; Score 402; DB 9; Length 453;
Best Local Similarity 99.8%; Pred. No. 1.2e-187;
Matches 452; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy   3690 GCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCT 3749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    453 GCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCT 394

Qy   3750 GGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCC 3809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    393 GGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCC 334

Qy   3810 CCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCCT 3869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    333 CCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCCT 274

Qy   3870 CTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGCCTGGCG 3929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    273 CTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGCCTGGCA 214

Qy   3930 AGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGTG 3989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    213 AGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGTG 154

Qy   3990 CTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTAA 4049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    153 CTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTAA 94

Qy   4050 AAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGA 4109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     93 AAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGA 34

Qy   4110 TGGAGATATTTACATGAATTGCATTTTACTTTA 4142
          ||||||||||||||||||||||||||||||||
Db     33 TGGAGATATTTACATGAATTGCATTTTACTTTA 1
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RESULT 4
AI652686/c

LOCUS	AI652686 455 bp mRNA linear EST 17-DEC-1999
DEFINITION	wb30f01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307193 3' similar to gb:X73029 NITRIC OXIDE SYNTHASE, INDUCIBLE (HUMAN);, mRNA sequence.
ACCESSION	AI652686
VERSION	AI652686.1 GI:4736665
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 455)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 563 Std Error: 0.00 Seq primer: -40UP from Gibco.

FEATURES Location/Qualifiers

source 1. .455
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2307193"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool

of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 124 a 100 c 120 g 111 t
ORIGIN

Query Match 9.6%; Score 396; DB 9; Length 455;
Best Local Similarity 99.8%; Pred. No. 1.2e-184;
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy   3693 GCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGG 3752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    455 GCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGG 396

Qy   3753 GAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCA 3812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    395 GAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCA 336

Qy   3813 TCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCCTCTC 3872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    335 TCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCCTCTC 276

Qy   3873 TCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGCCTGGCGAGT 3932
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    275 TCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGCCTGGCAAGT 216

Qy   3933 GGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGTGCTA 3992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    215 GGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGTGCTA 156

Qy   3993 TCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTAAAAA 4052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    155 TCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTAAAAA 96

Qy   4053 ACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGATGG 4112
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Db     95 ACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGATGG 36

Qy   4113 AGATATTTACATGAATTGCATTTTACT 4139
          |||||||||||||||||||||||||||
Db     35 AGATATTTACATGAATTGCATTTTACT 9
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RESULT 5
AI797675/c
LOCUS AI797675 445 bp mRNA linear EST 18-DEC-1999
DEFINITION we90c05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348360 3' similar to gb:X73029 NITRIC OXIDE SYNTHASE, INDUCIBLE (HUMAN);, mRNA sequence.
ACCESSION AI797675
VERSION AI797675.1 GI:5363147
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 445)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 514 Std Error: 0.00
Seq primer: -40UP from Gibco.
FEATURES Location/Qualifiers
source 1. .445
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2348360"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 125 a 96 c 116 g 108 t
ORIGIN

Query Match 9.5%; Score 392; DB 9; Length 445;
Best Local Similarity 99.8%; Pred. No. 1.1e-182;
Matches 442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy   3703 AACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGG 3762
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 AACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGG 386

Qy   3763 AAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTT 3822
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 AAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTT 326

Qy   3823 TACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGG 3882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 TACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGG 266

Qy   3883 GCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGA 3942
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    265 GCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGCCTGGCAAGTGGGTGAAAGA 206

Qy   3943 TGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACT 4002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 TGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACT 146

Qy   4003 GTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCC 4062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCC 86

Qy   4063 AGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTAC 4122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 AGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTAC 26

Qy   4123 ATGAATTGCATTTTACTTTAATC 4145
          |||||||||||||||||||||||
Db     25 ATGAATTGCATTTTACTTTAATC 3
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RESULT 6
BM834810
LOCUS BM834810 391 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0109948 S20T665307 Homo sapiens cDNA clone S20T665307-49-B07 5', mRNA sequence.
ACCESSION BM834810
VERSION BM834810.1 GI:19191219
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 391)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 49 row: B column: 07
High quality sequence stop: 391.

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FEATURES             Location/Qualifiers
     source          1. .391
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S20T665307-49-B07"
                     /clone_lib="S20T665307"
                     /sex="M"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
BASE COUNT       70 a    126 c    125 g     70 t
ORIGIN

  Query Match             8.4%;  Score 348;  DB 14;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-161;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    3167 GCCCTTCCGCAGTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGG 3226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      44 GCCCTTCCGCAGTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGG 103

Qy    3227 AGGCCGCATGACCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGA 3286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     104 AGGCCGCATGACCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGA 163

Qy    3287 GGAGATGCTGGAGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCG 3346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     164 GGAGATGCTGGAGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCG 223

Qy    3347 CCTGCCTGGCAAGCCCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGA 3406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     224 CCTGCCTGGCAAGCCCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGA 283

Qy    3407 GGTGCTCCGTGTGCTCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCAT 3466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     284 GGTGCTCCGTGTGCTCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCAT 343

Qy    3467 GGCCCGGGACGTGGCCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCT 3514
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     344 GGCCCGGGACGTGGCCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCT 391


RESULT 7
AW297448/c
LOCUS       AW297448                414 bp    mRNA    linear   EST 16-JAN-2000
DEFINITION  UI-H-BW0-ais-f-03-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone
            IMAGE:2730388 3', mRNA sequence.
ACCESSION   AW297448
VERSION     AW297448.1  GI:6704084
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            NCI-CGAP clone distribution information can be found through the
            T.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2730388"
                     /clone_lib="NCI_CGAP_Sub6"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub6
                     is a subtracted library derived from BW, which consists of
                     a  mixture of four normalized libraries: NCI_CGAP_Brn50,
                     NCI_CGAP_Lu13,  NCI_CGAP_Ov18, GBC1 . The NCI_CGAP_Sub6
                     library had 7 million recombinants.  A single-stranded DNA
                     preparation of BW was used as a tracer in a subtractive
                     hybridization with a driver comprising: the IMAGE pool
                     (NCI_CGAP_Kid3 pool 1  LLAM 3334-3337, 3682-3683,
                     3798-3803 (IMAGE CloneIDs 1322376-1323911,
                     1456008-1456775,1500552-1502855); NCI_CGAP_Kid5 pool 1
                     LLAM 3338-3342,3722-3725, 3776-3778 (IMAGE CloneIDs
                     1323912-1325831, 1471368-1472903, 1492104-1493255);
                     NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE
                     CloneIDs 1414920-1417991, 1520904-1522439); NCI_CGAP_GC4
                     pool 1 LLAM 3164-3167, 3716-3720, 3733-3735  (IMAGE
                     CloneIDs 1257096-1258631,1469064-1470983, 1475592-1476743
                     ); NCI_CGAP_Pr22 pool 1 LLAM 2457-2459, 2758-2759,
                     3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959,
                     1217928-1220615); NCI_CGAP_Co10 pool 1 LLAM 2644-2653,
                     2871-2872 (IMAGE CloneIDs 1057416-1061255,1144584-1145351
                     ). (50% of the driver  population), plus a pool of 3,840
                     arrayed clones from  NCI_CGAP_Sub1 (IMAGE  CloneIDs
                     2708616-2710535) and NCI_CGAP_Sub2 (IMAGE CloneIDs
                     2710536-2712455)    (20% of the driver population), plus a
                     pool of 11,136 clones from NCI_CGAP_Sub3  (IMAGE CloneIDs
                     2712456-2723591) (30% of the driver population).
                     Subtraction was performed as previously described [Bonaldo
                     , Lennon & Soares (1996): Normalization and  Subtraction:
                     Two Approaches To Facilitate Gene Discovery. Genome
                     Research 6, 791-806.
                     TAG_LIB=NCI_CGAP_Ov18
                     TAG_TISSUE=ovary
                     TAG_SEQ=GCGACA"
BASE COUNT       115 a     83 c    105 g    111 t
ORIGIN

  Query Match             8.3%;  Score 346;  DB 10;  Length 414;
  Best Local Similarity   99.7%;  Pred. No. 7.3e-160;
  Matches  396;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    3749 TGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTC 3808
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     414 TGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTC 355

Qy    3809 CCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCC 3868
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     354 CCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCC 295
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Qy   3869 TCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGCCTGGC 3928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    294 TCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGCCTGGC 235

Qy   3929 GAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGT 3988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    234 AAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGT 175

Qy   3989 GCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTA 4048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    174 GCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTA 115

Qy   4049 AAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTG 4108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    114 AAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTG 55

Qy   4109 ATGGAGATATTTACATGAATTGCATTTTACTTTAATC 4145
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Db     54 ATGGAGATATTTACATGAATTGCATTTTACTTTAATC 18
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RESULT 8
AW236981/c
LOCUS AW236981 516 bp mRNA linear EST 13-DEC-1999
DEFINITION xm51f11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2687757 3' similar to gb:X73029 NITRIC OXIDE SYNTHASE, INDUCIBLE (HUMAN);, mRNA sequence.
ACCESSION AW236981
VERSION AW236981.1 GI:6569370
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 516)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 331.

FEATURES Location/Qualifiers
source 1. .516
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2687757"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 139 a 122 c 131 g 124 t
ORIGIN

Query Match 8.3%; Score 344; DB 10; Length 516;
Best Local Similarity 99.7%; Pred. No. 7.6e-159;
Matches 394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy   3725 TGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCA 3784
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 TGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCA 364

Qy   3785 AGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAG 3844
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 AGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAG 304

Qy   3845 CACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGAC 3904
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Db    303 CACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGAC 244

Qy   3905 AAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCAC 3964
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    243 AAAATCTTAAATGCCAGGCCTGGCAAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCAC 184

Qy   3965 CACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTA 4024
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Db    183 CACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTA 124

Qy   4025 CAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTT 4084
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 CAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTT 64

Qy   4085 GGGTCTTCCCTGTATGATTCCTTGATGGAGATATT 4119
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Db     63 GGGTCTTCCCTGTATGATTCCTTGATGGAGATATT 29
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RESULT 9
BF375262
LOCUS BF375262 513 bp mRNA linear EST 24-NOV-2000
DEFINITION QV0-ST0215-061299-065-h11 ST0215 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF375262
VERSION BF375262.1 GI:11337287
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 513)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV0&t2=QV0-ST0215-061299-065-h11&t3=1999-12-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 33
High quality sequence stop: 51.

FEATURES Location/Qualifiers
source 1. .513
/organism="Homo sapiens"

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                     /db_xref="taxon:9606"
                     /clone_lib="ST0215"
                     /dev_stage="Adult"
                     /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      116 a    135 c    152 g    110 t
ORIGIN

  Query Match             8.2%;  Score 339;  DB 12;  Length 513;
  Best Local Similarity   99.7%;  Pred. No. 2.3e-156;
  Matches  389;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    3407 GGTGCTCCGTGTGCTCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCAT 3466
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Db      76 GGTGCTCCGTGTGCTCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCAT 135

Qy    3467 GGCCCGGGACGTGGCCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGA 3526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     136 GGCCCGGGACGTGGCCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGA 195

Qy    3527 GGAGCAGGTCGAGGACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATAT 3586
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     196 GGAGCAGGTCGAGGACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATAT 255

Qy    3587 CTTCGGTGCTGTATTTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAG 3646
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     256 CTTTGGTGCTGTATTTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAG 315

Qy    3647 CCTGGAGATGTCAGCGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACT 3706
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 CCTGGAGATGTCAGCGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACT 375

Qy    3707 TAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAG 3766
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Db     376 TAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAG 435

Qy    3767 TGATATCCCCCAGCCTCAAGTCTTATTTCC 3796
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Db     436 TGATATCCCCCAGCCTCAAGTCTTATTTCC 465


RESULT 10
AW950935
LOCUS       AW950935                 621 bp    mRNA    linear   EST 01-JUN-2000
DEFINITION  EST363005 MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW950935
VERSION     AW950935.1  GI:8140599
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
            ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
  TITLE     Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
  JOURNAL   Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 21
            Seq primer: Reverse.
FEATURES             Location/Qualifiers
     source          1. .621
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="MAGE resequences, MAGA"
                     /note="Vector: pBluescriptSKm"
BASE COUNT      122 a    224 c    162 g    113 t
ORIGIN

  Query Match             7.3%;  Score 301;  DB 10;  Length 621;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-137;
  Matches  301;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2702 GGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAGA 2761
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79 GGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAGA 138

Qy    2762 AGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGAA 2821
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     139 AGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGAA 198

Qy    2822 GTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGTC 2881
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Db     199 GTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGTC 258

Qy    2882 TGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCTC 2941
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Db     259 TGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCTC 318

Qy    2942 CTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACAC 3001
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     319 CTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACAC 378

Qy    3002 C 3002
           |
Db     379 C 379


RESULT 11
AW445097/c
LOCUS       AW445097                 364 bp    mRNA    linear   EST 17-FEB-2000
DEFINITION  UI-H-BI3-akd-e-12-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone
            IMAGE:2733815 3', mRNA sequence.
ACCESSION   AW445097
VERSION     AW445097.1  GI:6986859
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 364)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            NCI-CGAP clone distribution information can be found through the
            I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2733815"
                     /clone_lib="NCI_CGAP_Sub5"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
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                     polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub5
                     is a subtracted library derived from NCI_CGAP_Sub4. The
                     NCI_CGAP_Sub5 library had 3 million recombinants. A
                     single-stranded DNA preparation of NCI_CGAP_Sub4 was used
                     as a tracer in a subtractive  hybridization with a driver
                     comprising: the IMAGE pool (NCI_CGAP_Kid3 pool 1 LLAM
                     3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs
                     1322376-1323911, 1456008-1456775,1500552-1502855);
                     NCI_CGAP_Kid5 pool 1 LLAM 3338-3342,3722-3725, 3776-3778
                     (IMAGE CloneIDs 1323912-1325831, 1471368-1472903,
                     1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582,
                     3851-3854 (IMAGE  CloneIDs 1414920-1417991,1520904-1522439
                     ); NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720,
                     3733-3735 (IMAGE CloneIDs 1257096-1258631,1469064-1470983,
                     1475592-1476743); NCI_CGAP_Pr22  pool 1 LLAM 2457-2459,
                     2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759
                     ,1101192-1101959,  1217928-1220615); NCI_CGAP_Co10 pool 1
                     LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs  1057416-1061255
                     ,1144584-1145351). (10% of the driver population), plus a
                     pool of 3,840  arrayed clones from  NCI_CGAP_Sub1 (IMAGE
                     CloneIDs 2708616-2710535) and  NCI_CGAP_Sub2 (IMAGE
                     CloneIDs 2710536-2712455)   (10% of the driver population
                     ), plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE
                     CloneIDs 2712456-2723591) (10% of the driver population),
                     plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE
                     CloneIDs 2723592-2728969) (70% of the driver population).
                     Subtraction was performed as previously described [Bonaldo
                     , Lennon & Soares (1996): Normalization and Subtraction:
                     Two Approaches To Facilitate Gene Discovery. Genome
                     Research 6, 791-806.
                     TAG_LIB=NCI_CGAP_Co10
                     TAG_TISSUE=colon
                     TAG_SEQ=AAACG"
BASE COUNT      102 a     70 c     93 g     99 t
ORIGIN

  Query Match             7.1%;  Score 296;  DB 10;  Length 364;
  Best Local Similarity   99.7%;  Pred. No. 4.5e-135;
  Matches  346;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   3799 AACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGAT 3858
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Db    364 AACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGAT 305

Qy   3859 CGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGC 3918
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 CGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGC 245

Qy   3919 CAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACC 3978
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 CAGGCCTGGCAAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACC 185

Qy   3979 ACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCC 4038
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 ACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCC 125

Qy   4039 TCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTA 4098
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 TCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTA 65

Qy   4099 TGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTTTAATC 4145
           |||||||||||||||||||||||||||||||||||||||||||||
Db     64 TGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTTTAATC 18


RESULT 12
AW449618/c
LOCUS       AW449618                 355 bp    mRNA    linear   EST 17-FEB-2000
DEFINITION  UI-H-BI3-aku-h-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone
            IMAGE:2735846 3', mRNA sequence.
ACCESSION   AW449618
VERSION     AW449618.1  GI:6990324
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 355)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            NCI-CGAP clone distribution information can be found through the
            I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html The following repetitive
            elements were found in this cDNA sequence: 1-27,
            >AT_rich#Low_complexity
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .355
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2735846"
                     /clone_lib="NCI_CGAP_Sub5"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub5
                     is a subtracted library derived from NCI_CGAP_Sub4. The
                     NCI_CGAP_Sub5 library had 3 million recombinants. A
                     single-stranded DNA preparation of NCI_CGAP_Sub4 was used
                     as a tracer in a subtractive  hybridization with a driver
                     comprising: the IMAGE pool (NCI_CGAP_Kid3 pool 1 LLAM
                     3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs
                     1322376-1323911, 1456008-1456775,1500552-1502855);
                     NCI_CGAP_Kid5 pool 1 LLAM 3338-3342,3722-3725, 3776-3778
                     (IMAGE CloneIDs 1323912-1325831, 1471368-1472903,
                     1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582,
                     3851-3854 (IMAGE  CloneIDs 1414920-1417991,1520904-1522439
                     ); NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720,
                     3733-3735 (IMAGE CloneIDs 1257096-1258631,1469064-1470983,
                     1475592-1476743); NCI_CGAP_Pr22  pool 1 LLAM 2457-2459,
                     2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759
                     ,1101192-1101959,  1217928-1220615); NCI_CGAP_Co10 pool 1
                     LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs  1057416-1061255
                     ,1144584-1145351). (10% of the driver population), plus a
                     pool of 3,840  arrayed clones from  NCI_CGAP_Sub1 (IMAGE
                     CloneIDs 2708616-2710535) and  NCI_CGAP_Sub2 (IMAGE
                     CloneIDs 2710536-2712455)   (10% of the driver population
                     ), plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE
                     CloneIDs 2712456-2723591) (10% of the driver population),
                     plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE
                     CloneIDs 2723592-2728969) (70% of the driver population).
                     Subtraction was performed as previously described [Bonaldo
                     , Lennon & Soares (1996): Normalization and Subtraction:
                     Two Approaches To Facilitate Gene Discovery. Genome
                     Research 6, 791-806.
                     TAG_LIB=NCI_CGAP_Co10
                     TAG_TISSUE=colon
                     TAG_SEQ=AAACG"
BASE COUNT      100 a     69 c     90 g     96 t
ORIGIN

  Query Match             7.0%;  Score 289;  DB 10;  Length 355;
  Best Local Similarity   99.7%;  Pred. No. 1.3e-131;
  Matches  339;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   3804 TGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAG 3863
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    355 TGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAG 296
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Qy   3864 CCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGC 3923
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Db    295 CCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGC 236

Qy   3924 CTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAG 3983
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 CTGGCAAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAG 176

Qy   3984 GAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGT 4043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    175 GAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGT 116

Qy   4044 ATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATT 4103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    115 ATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATT 56

Qy   4104 CCTTGATGGAGATATTTACATGAATTGCATTTTACTTTAA 4143
          |||||||||||||||||||||||||||||||||||||||
Db     55 CCTTGATGGAGATATTTACATGAATTGCATTTTACTTTAA 16
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RESULT 13
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LOCUS       AW391328                541 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  QV0-ST0215-061299-065-f03 ST0215 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW391328
VERSION     AW391328.1  GI:6896091
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 541)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV0&t2=QV0-ST0215-
            061299-065-f03&t3=1999-12-06&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 68
            High quality sequence stop: 541.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone_lib="ST0215"
                     /dev_stage="Adult"
                     /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      127 a    139 c    155 g    120 t
ORIGIN
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Qy   3407 GGTGCTCCGTGTGCTCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCAT 3466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     92 GGTGCTCCGTGTGCTCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCAT 151

Qy   3467 GGCCCGGGACGTGGCCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGA 3526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    152 TGCCCGGGACGTGGCCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGA 211

Qy   3527 GGAGCAGGTCGAGGACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATAT 3586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    212 GGAGCAGGTCGAGGACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATAT 271

Qy   3587 CTTCGGTGCTGTATTTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAG 3646
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Db    272 CTTTGGTGCTGTATTTCCTTACGAGGCGAAGAAGGACAGAGTGGCGGTGCAGCCCAGCAG 331

Qy   3647 CCTGGAGATGTCAGCGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACT 3706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    332 CCTGGAGATGTCAGCGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACT 391

Qy   3707 TAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAG 3766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    392 TAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAG 451

Qy   3767 TGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACT 3826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    452 TGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACT 511

Qy   3827 TG 3828
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Db    512 TG 513
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RESULT 14
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LOCUS       AW950112                377 bp    mRNA    linear   EST 01-JUN-2000
DEFINITION  EST362077 MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW950112
VERSION     AW950112.1  GI:8139648
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 377)
  AUTHORS   Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
            ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
  TITLE     Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
  JOURNAL   Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 9
            Seq primer: Reverse.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="MAGE resequences, MAGA"
                     /note="Vector: pBluescriptSKm"
BASE COUNT       78 a    132 c     96 g     71 t
ORIGIN
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  Best Local Similarity   100.0%;  Pred. No. 8e-103;
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Db     64 TCCAAAAGCTGGCCCAGGTGGCCACAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGT 123

Qy   2794 GCCAGCCCTCAGAGTACAGCAAGTGGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGC 2853
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 GCCAGCCCTCAGAGTACAGCAAGTGGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGC 183

Qy   2854 TAGAGGAGTTCCCGTCCCTGCGGGTGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTC 2913
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 TAGAGGAGTTCCCGTCCCTGCGGGTGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTC 243

Qy   2914 TGAAGCCCAGGTTCTACTCCATCAGCTCCTCCCGGGATCACACGCCCACGG 2964
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 TGAAGCCCAGGTTCTACTCCATCAGCTCCTCCCGGGATCACACGCCCACGG 294


RESULT 15
AI493548/c
LOCUS       AI493548                245 bp    mRNA    linear   EST 11-MAR-1999
DEFINITION  th36b03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120333 3'
            similar to gb:X73029 NITRIC OXIDE SYNTHASE, INDUCIBLE (HUMAN);,
            mRNA sequence.
ACCESSION   AI493548
VERSION     AI493548.1  GI:4394551
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 245)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
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                     /clone_lib="NCI_CGAP_Pan1"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.72 kb. Life Technologies catalog #:
                     11548-013"
BASE COUNT       74 a     52 c     61 g     58 t
ORIGIN

  Query Match             5.2%;  Score 216;  DB 9;  Length 245;
  Best Local Similarity   100.0%;  Pred. No. 2e-95;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3930 AGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGTG 3989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220 AGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGTG 161

Qy   3990 CTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTAA 4049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160 CTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTAA 101

Qy   4050 AAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGA 4109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    100 AAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGA 41

Qy   4110 TGGAGATATTTACATGAATTGCATTTTACTTTAATC 4145
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Db     40 TGGAGATATTTACATGAATTGCATTTTACTTTAATC 5


Search completed: March 14, 2003, 10:17:24
Job time : 5428 secs
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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 08:40:48 ; Search time 134 Seconds
(without alignments)
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Title: US-09-490-208-3
Perfect score: 4145
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 50

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4145	100.0	4145	1	US-08-314-917-1	Sequence 1, Appli
2	4145	100.0	4145	1	US-08-265-046-1	Sequence 1, Appli
3	4145	100.0	4145	2	US-08-465-522-1	Sequence 1, Appli
4	4145	100.0	4145	5	PCT-US93-11401-1	Sequence 1, Appli
5	4145	100.0	4145	5	PCT-US95-07849-1	Sequence 1, Appli
6	3381	81.6	4062	4	US-09-126-109-11	Sequence 11, Appl
7	585	14.1	604	4	US-09-068-880-1	Sequence 1, Appli
8	480	11.6	1026	4	US-09-068-880-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-314-917-1
; Sequence 1, Application US/08314917
; Patent No. 5468630
; GENERAL INFORMATION:
; APPLICANT: Billiar, Timothy R.
; APPLICANT: Nussler, Andreas K.
; APPLICANT: Geller, David A.
; APPLICANT: Simmons, Richard L.
; TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric
; TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold B. Silverman
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 600 Grant Street, 42nd Floor
; CITY: Pittsburgh
; STATE: PA
; COUNTRY: USA
; ZIP: 15219
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,917
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/981,344
; FILING DATE: 25-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Arnold B.
; REGISTRATION NUMBER: 22,614
; REFERENCE/DOCKET NUMBER: 116972
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (412) 566-6000
; TELEFAX: (412) 566-6099
; TELEX: 866172
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
; DESCRIPTION: Synthase cDNA Clone
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Induced Human Hepatocyte RNA
; IMMEDIATE SOURCE:
; LIBRARY: Lambda Zap II cDNA
; CLONE: pHINOS
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: unknown
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..3668
; IDENTIFICATION METHOD: Experiment
US-08-314-917-1

Query Match 100.0%; Score 4145; DB 1; Length 4145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
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Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
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Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
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Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
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Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
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Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
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Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
Db    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
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Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
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Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
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Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
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Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
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Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
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Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
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Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
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Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
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Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
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Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
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Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
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Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
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Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
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Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
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Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
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Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
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Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
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Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
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Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
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Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
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Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
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Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
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Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
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Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
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Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
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Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
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Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
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Qy   4141 TAATC 4145
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Db   4141 TAATC 4145
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RESULT 2
US-08-265-046-1
; Sequence 1, Application US/08265046
; Patent No. 5658565
;  GENERAL INFORMATION:
;    APPLICANT:  Timothy R. Billiar
;    APPLICANT:  Edith Tzeng
;    APPLICANT:  Andreas K. Nussler
;    APPLICANT:  David A. Geller
;    APPLICANT:  Richard L. Simmons
;    TITLE OF INVENTION:  Inducible Nitric Oxide Synthase
;    TITLE OF INVENTION:  Gene for Treatment of Disease
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lewis F. Gould, Jr.
;      ADDRESSEE:  Eckert Seamans Cherin & Mellott
;      STREET:  1700 Market Street, Suite 3232
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,046
```

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;      FILING DATE:  24-JUN-1994
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gould, Lewis F. Jr.
;      REGISTRATION NUMBER:  25,057
;      REFERENCE/DOCKET NUMBER:  119130
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 575-6020
;      TELEFAX:  (215) 575-6015
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4145 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;      DESCRIPTION:  Human Hepatocyte Inducible Nitric Oxide
;      DESCRIPTION:  Synthase cDNA Clone
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      TISSUE TYPE:  Induced Human Hepatocyte RNA
;    IMMEDIATE SOURCE:
;      LIBRARY:  Lambda Zap II cDNA
;      CLONE:  pHINOS
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  unknown
;      MAP POSITION:  unknown
;      UNITS:  unknown
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  207..3668
;      IDENTIFICATION METHOD:  Experiment
US-08-265-046-1

  Query Match             100.0%;  Score 4145;  DB 1;  Length 4145;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
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Db      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

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Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
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Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
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Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
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Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
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Db    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

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Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

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Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
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Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
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Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
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Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
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Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
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Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
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Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
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Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
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Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
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Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
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Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
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Db  1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy  1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
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Db  1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy  1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy  1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
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Db  1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy  1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy  1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy  1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy  1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy  2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
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Db  2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy  2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
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Qy  2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
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Qy  2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
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Qy  2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
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Db  2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy  2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
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Db  2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy  2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
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Db  2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy  2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
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Qy  2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
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Qy  2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
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Db  2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

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Qy  2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy  2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
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Qy  3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
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Qy  3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
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Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
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Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
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RESULT 3
US-08-465-522-1
; Sequence 1, Application US/08465522
; Patent No. 5882908
;  GENERAL INFORMATION:
;    APPLICANT:  Billiar, Timothy R.
;    APPLICANT:  Nussler, Andreas K.
;    APPLICANT:  Geller, David A.
;    APPLICANT:  Simmons, Richard L.
;    TITLE OF INVENTION:  cDNA Clone for Human Inducible Nitric
;    TITLE OF INVENTION:  Oxide Synthase And Process for Preparing Same
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lewis F. Gould, Jr.
;      ADDRESSEE:  Eckert Seamans Cherin & Mellott
;      STREET:  1700 Market St. Suite 3232
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,522
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gould, Jr., Lewis F.
;      REGISTRATION NUMBER:  25,057
;      REFERENCE/DOCKET NUMBER:  116972-6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 575-6020
;      TELEFAX:  (215) 575-6015
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4145 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;      DESCRIPTION:  Human Hepatocyte Inducible Nitric Oxide
;      DESCRIPTION:  Synthase cDNA Clone
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      TISSUE TYPE:  Induced Human Hepatocyte RNA
;    IMMEDIATE SOURCE:
;      LIBRARY:  Lambda Zap II cDNA
;      CLONE:  pHINOS
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  unknown
;      MAP POSITION:  unknown
;      UNITS:  unknown
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  207..3668
;      IDENTIFICATION METHOD:  Experiment
US-08-465-522-1

  Query Match             100.0%;  Score 4145;  DB 2;  Length 4145;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
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Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
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Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
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Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
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Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
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Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
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Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
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Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
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Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
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Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
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Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
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Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
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Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
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Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
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Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
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RESULT 4
PCT-US93-11401-1
; Sequence 1, Application PCTUS9311401
; GENERAL INFORMATION:
; APPLICANT: Billiar, Timothy R.
; APPLICANT: Nussler, Andreas K.
; APPLICANT: Geller, David A.
; APPLICANT: Simmons, Richard L.
; TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric
; TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold B. Silverman
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 600 Grant Street, 42nd Floor
; CITY: Pittsburgh
; STATE: PA
; COUNTRY: USA
; ZIP: 15219
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11401
; FILING DATE: 25-NOV-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/981,344
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Arnold B.
; REGISTRATION NUMBER: 22,614
; REFERENCE/DOCKET NUMBER: 116972
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (412) 566-6000
; TELEFAX: (412) 566-6099
; TELEX: 866172
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Induced Human Hepatocyte RNA
; IMMEDIATE SOURCE:
; LIBRARY: Lambda Zap II cDNA
; CLONE: pHINOS
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: unknown
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..3668
; IDENTIFICATION METHOD: Experiment

/CT-US93-11401-1

Query Match 100.0%; Score 4145; DB 5; Length 4145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
Db     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
Db     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
Db     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
Db     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
Db     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
Db     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
Db     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
Db     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
Db     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
Db     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
Db     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
Db     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
Db     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
Db     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
Db    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
Db    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
Db    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
Db    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
Db    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Db    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Db    1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Db    1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Db    1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560

Qy    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Db    1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Db    1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy    1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Db    1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy    1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Db    1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy    1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Db    1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy    1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Db    1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy    1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Db    1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy    1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Db    1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy    2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Db    2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
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Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
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Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
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Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
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Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
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RESULT 5
PCT-US95-07849-1
; Sequence 1, Application PC/TUS9507849
; GENERAL INFORMATION:
; APPLICANT: University of Pittsburgh of the Commonwealth System of Higher

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;    APPLICANT:  Education
;    TITLE OF INVENTION:  Inducible Nitric Oxide Synthase
;    TITLE OF INVENTION:  Gene for Treatment of Disease
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lewis F. Gould, Jr.
;      ADDRESSEE:  Eckert Seamans Cherin & Mellott
;      STREET:  1700 Market Street, Suite 3232
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/07849
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gould, Lewis F. Jr.
;      REGISTRATION NUMBER:  25,057
;      REFERENCE/DOCKET NUMBER:  119130-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 575-6020
;      TELEFAX:  (215) 575-6015
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4145 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;      DESCRIPTION:  Human Hepatocyte Inducible Nitric Oxide
;      DESCRIPTION:  Synthase cDNA Clone
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      TISSUE TYPE:  Induced Human Hepatocyte RNA
;    IMMEDIATE SOURCE:
;      LIBRARY:  Lambda Zap II cDNA
;      CLONE:  pHINOS
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  unknown
;      MAP POSITION:  unknown
;      UNITS:  unknown
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  207..3668
;      IDENTIFICATION METHOD:  Experiment
PCT-US95-07849-1

  Query Match             100.0%;  Score 4145;  DB 5;  Length 4145;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
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Db     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
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Db     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
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Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
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Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
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Db   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620

Qy   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680

Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
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Db   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740

Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980

Qy   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040

Qy   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100

Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160

Qy   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220

Qy   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280

Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580

Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700

Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760

Qy   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
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Db   2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820

Qy   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880

Qy   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940

Qy   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

Qy   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300

Qy   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360

Qy   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420

Qy   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480

Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
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Db    3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Qy    3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Db    3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy    3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Db    3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy    3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Db    3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy    3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Db    3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy    3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Db    3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy    3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Db    3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy    3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Db    3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy    3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Db    3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Db    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Db    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy    4141 TAATC 4145

Db    4141 TAATC 4145


RESULT 6
US-09-126-109-11
; Sequence 11, Application US/09126109
; Patent No. 6171856
;  GENERAL INFORMATION:
;     APPLICANT:  Thigpen, Anice
;     APPLICANT:  Hohmeier, Hans-Ewald
;     APPLICANT:  Newgard, Christopher B.
;     APPLICANT:  Unger, Roger H.
;     APPLICANT:  Shimabukuro, Michio
;     APPLICANT:  Chen, Guaxun
;     APPLICANT:  Rhodes, Christopher J.
;     APPLICANT:  Hugl, Sigrun R.
;     APPLICANT:  Cousin, Sharon
;     TITLE OF INVENTION:  METHODS AND COMPOSITIONS RELATING
;     TITLE OF INVENTION:  TO NO-MEDIATED CYTOTOXICITY
;     NUMBER OF SEQUENCES:  20
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Arnold, White & Durkee
;       STREET:  P.O. Box 4433
;       CITY:  Houston
;       STATE:  Texas
;       COUNTRY:  USA
;       ZIP:  77210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/126,109
;       FILING DATE:  30-JUL-1998
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/055,092
;       FILING DATE:  30-JUL-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US Unknown
;       FILING DATE:  03-MAR-1998
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McMillian, Nabeela R.
;       REGISTRATION NUMBER:  P-43,363
;       REFERENCE/DOCKET NUMBER:  UTSD:560
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (512) 418-3000
;       TELEFAX:  (512) 474-7577
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4062 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-09-126-109-11

  Query Match             81.6%;  Score 3381;  DB 4;  Length 4062;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 4031;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy     102 TACCCCGGGGAGGCAGTGCAGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAA 161

Db       1 TACCCCGGGGAGGCAGTGCAGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAA 60

Qy     162 ATCCAGATAAGTGACATAAGTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGG 221

Db      61 ATCCAGATAAGTGACATAAGTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGG 120

Qy     222 AAATTTCTGTTCAAGACCAAATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAAC 281

Db     121 AAATTTCTGTTCAAGACCAAATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAAC 180

Qy     282 AACAATGTGGAGAAAGCCCCCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAG 341

Db     181 AACAATGTGGAGAAAGCCCCCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAG 240

Qy     342 TATCACAACCTCAGCAAGCAGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAG 401

Db     241 TATCACAACCTCAGCAAGCAGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAG 300

Qy     402 AAGTCTCCAGAATCTCTGGTCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTG 461

Db     301 AAGTCTCCAGAATCTCTGGTCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTG 360

Qy     462 AGGATCAAAAACTGGGGCAGCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAA 521

Db     361 AGGATCAAAAACTGGGGCAGCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAA 420

Qy     522 GGGATTTTAACTTGCAGGTCCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTG 581

Db     421 GGGATTTTAACTTGCAGGTCCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTG 480

Qy     582 ACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAA 641

Db     481 ACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAA 540

Qy     642 TTTGTCAACCAATATTACGGCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGG 701

Db     541 TTTGTCAACCAATATTACGGCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGG 600
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Qy    702 GTGGAAGCGGTAACAAAGGAGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAG 761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTGGAAGCGGTAACAAAGGAGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAG 660

Qy    762 CTCATCTTCGCCACCAAGCAGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAG 821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCATCTTCGCCACCAAGCAGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAG 720

Qy    822 TGGTCCAACCTGCAGGTCTTCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAA 881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TGGTCCAACCTGCAGGTCTTCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAA 780

Qy    882 CACATCTGCAGACACGTGCGTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACC 941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CACATCTGCAGACACGTGCGTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACC 840

Qy    942 GTGTTCCCCCAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATC 1001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GTGTTCCCCCAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATC 900

Qy   1002 CGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAA 1061
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Db    901 CGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAA 960

Qy   1062 TTCACTCAGCTGTGCATCGACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTC 1121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTCACTCAGCTGTGCATCGACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTC 1020

Qy   1122 CCCCTGGTCCTGCAGGCCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTT 1181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCCCTGGTCCTGCAGGCCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTT 1080

Qy   1182 GTGCTTGAGGTGGCCATGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAG 1241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GTGCTTGAGGTGGCCATGGAACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAG 1140

Qy   1242 TGGTACGCCCTGCCTGCAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCA 1301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TGGTACGCCCTGCCTGCAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCA 1200

Qy   1302 GGGTGCCCCTTCAATGGCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGAC 1361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGGTGCCCCTTCAATGGCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGAC 1260

Qy   1362 GTCCAGCGCTACAACATCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAG 1421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTCCAGCGCTACAACATCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAG 1320

Qy   1422 CTGGCCTCGCTCTGGAAAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGT 1481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CTGGCCTCGCTCTGGAAAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGT 1380

Qy   1482 TTTCAGAAGCAGAATGTGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAG 1541
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TTCCAGAAGCAGAATGTGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAG 1440

Qy   1542 TACATGCAGAATGAATACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTC 1601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TACATGCAGAATGAATACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTC 1500

Qy   1602 CCTCCCATGTCTGGGAGCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTG 1661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCTCCCATGTCTGGGAGCATCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTG 1560

Qy   1662 TCCCCTTTCTACTACTATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAG 1721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCCCCTTTCTACTACTATCAGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAG 1620

Qy   1722 CGGAGACCCAAGAGAAGAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCC 1781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CGGAGACCCAAGAGAAGAGAGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCC 1680

Qy   1782 TGTATGCTGATGCGCAAGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACA 1841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TGTATGCTGATGCGCAAGACAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACA 1740

Qy   1842 GAGACAGGAAAATCAGAGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTC 1901
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Db   1741 GAGACAGGAAAATCAGAGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTC 1800

Qy   1902 AACCCCAAGGTTGTCTGCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTG 1961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACCCCAAGGTTGTCTGCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTG 1860

Qy   1962 CTGTTGGTGGTGACCAGTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTG 2021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CTGTTGGTGGTGACCAGTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTG 1920

Qy   2022 AAGAAATCGCTCTTCATGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGC 2081
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 AAGAAATTGCTCTTCATGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGC 1980

Qy   2082 CTCGGCTCCAGCATGTACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTG 2141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CTCGGCTCCAGCATGTACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTG 2040

Qy   2142 TCCCACCTGGGGGCCTCTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAG 2201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TCCCACCTGGGGGCCTCTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAG 2100

Qy   2202 GAGGACGCCTTCCGCAGCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGAT 2261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GAGGACGCCTTCCGCAGCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGAT 2160

Qy   2262 GTCCGAGGCAAACAGCACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGAC 2321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GTCCGAGGCAAACAGCACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGAC 2220

Qy   2322 CCGCACCACTACAGGCTCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGC 2381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CCGCACCACTACAGGCTCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGC 2280

Qy   2382 AGCATGCATGCCAAGAACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGT 2441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AGCATGCATGCCAAGAACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGT 2340

Qy   2442 CCGACATCCAGCCGTGCCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTG 2501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCGACATCCAGCCGTGCCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTG 2400

Qy   2502 AACTACCTGCCGGGGGGAGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAA 2561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 AACTACCTGCCGGGGGGAGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAA 2460

Qy   2562 GGCATCCTGGAGCGAGTGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGAC 2621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   2461 GGCATCCTGGAGCGAGTGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCC 2520

Qy   2622 CTGGATGAGAGTGGCAGCTACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGC 2681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 CTGGATGAGAGTGGCAGCTACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGC 2580

Qy   2682 CAGGCCCTCACCTACTCCCCGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAG 2741
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Qy   2742 CTGGCCCAGGTGGCCACAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCC 2801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 CTGGCCCAGGTGGCCACAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCC 2700

Qy   2802 TCAGAGTACAGCAAGTGGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAG 2861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TCAGAGTACAGCAAGTGGAAGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAG 2760

Qy   2862 TTCCCGTCCCTGCGGGTGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCC 2921
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Db   2761 TTCCCGTCCCTGCGGGTGTCTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCC 2820

Qy   2922 AGGTTCTACTCCATCAGCTCCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTG 2981
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AGGTTCTACTCCATCAGCTCCTCCCGGGATCACACGCCCACAGAGATCCACCTGACTGTG 2880

Qy   2982 GCCGTGGTCACCTACCACACCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGC 3041
          |||||||||||||||||||| ||||||||||||||||||||||||||||||| |||||||||
Db   2881 GCCGTGGTCACCTACCACACCCGAGATGGCCAGGGTCCCCTGCACCACGGCGTCTGCAGC 2940

Qy   3042 ACATGGCTCAACAGCCTGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGC 3101
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 ACATGGCTCAACAGCCTGAAGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGC 3000

Qy   3102 GCCTTCCACCTCCCCGAGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGC 3161
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GGCTTCCACCTCCCCGAGGATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGC 3060

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          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 ATCGCGCCCTTCCGCAGTTTCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTG 3120

Qy   3222 CGGGGAGGCCGCATGACCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTAC 3281
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 CGGGGAGGCCGCATGACCTTGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTAC 3180

Qy   3282 CAGGAGGAGATGCTGGAGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTAT 3341
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CAGGAGGAGATGCTGGAGATGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTAT 3240

Qy   3342 TCCCGCCTGCCTGGCAAGCCCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCC 3401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TCCCGCCTGCCTGGCAAGCCCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCC 3300

Qy   3402 AGCGAGGTGCTCCGTGTGCTCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTG 3461
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 AGCGAGGTGCTCCGTGTGCTCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTG 3360

Qy   3462 CGCATGGCCCGGGACGTGGCCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTG 3521
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CGCATGGCCCGGGACGTGGCCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTG 3420

Qy   3522 AATGAGGAGCAGGTCGAGGACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAA 3581
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AATGAGGAGCAGGTCGAGGACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAA 3480

Qy   3582 GATATCTTCGGTGCTGTATTTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCC 3641
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GATATCTTTGGTGCTGTATTTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCC 3540

Qy   3642 AGCAGCCTGGAGATGTCAGCGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACA 3701
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 AGCAGCCTGGAGATGTCAGCGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACA 3600

Qy   3702 GAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAG 3761
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Db   3601 GAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAG 3660

Qy   3762 GAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCT 3821
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Db   3661 GAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCT 3720

Qy   3822 TTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGG 3881
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Db   3721 TTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGG 3780

Qy   3882 GGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAG 3941
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Qy   3942 ATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCAC 4001
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Db   3841 ATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCAC 3900

Qy   4002 TGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACC 4061
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Qy   4062 CAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTA 4121
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Qy   4122 CATGAATTGCATTTTACTTTAATC 4145
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Db   4021 CATGAATTGCATTTTACTTTAATC 4044
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RESULT 7
US-09-068-880-1
; Sequence 1, Application US/09068880B
; Patent No. 6203982
; GENERAL INFORMATION:
; APPLICANT: Nunokawa, Youichi
; APPLICANT: Oikawa, Shinzo
; APPLICANT: Tanaka, Shoji
; TITLE OF INVENTION: Method for Screening Compounds
; TITLE OF INVENTION: Regulating the Expression of Human-Inducible Nitric Oxide
; TITLE OF INVENTION: Synthase
; FILE REFERENCE: SHIM-001
; CURRENT APPLICATION NUMBER: US/09/068,880B
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: PCT/JP97/03303
; EARLIER FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-068-880-1

Query Match 14.1%; Score 585; DB 4; Length 604;
Best Local Similarity 100.0%; Pred. No. 9.9e-271;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   3561 AGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTATTTCCTTACGAGGCGAAGAAG 3620
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Db      1 AGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTATTTCCTTACGAGGCGAAGAAG 60

Qy   3621 GACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAGCGCTCTGAGGGCCTACAGGA 3680
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Db     61 GACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAGCGCTCTGAGGGCCTACAGGA 120

Qy   3681 GGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTC 3740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTC 180

Qy   3741 ACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAA 3800
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Db    181 ACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAA 240

Qy   3801 CGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCG 3860
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Qy   3861 GAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCA 3920
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Qy   3921 GGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCAC 3980
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Qy   3981 CAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTC 4040
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Db    421 CAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTACAGTTATTTATGCCTC 480

Qy   4041 TGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATG 4100
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Db    481 TGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTGGGTCTTCCCTGTATG 540

Qy   4101 ATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTTTAATC 4145
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Db    541 ATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTTTAATC 585


RESULT 8
US-09-068-880-14
; Sequence 14, Application US/09068880B
; Patent No. 6203982
; GENERAL INFORMATION:
;  APPLICANT: Nunokawa, Youichi
;  APPLICANT: Oikawa, Shinzo
;  APPLICANT: Tanaka, Shoji
;  TITLE OF INVENTION: Method for Screening Compounds
;  TITLE OF INVENTION: Regulating the Expression of Human-Inducible Nitric Oxide
;  TITLE OF INVENTION: Synthase
;  FILE REFERENCE: SHIM-001
;  CURRENT APPLICATION NUMBER: US/09/068,880B
;  CURRENT FILING DATE: 1998-09-02
;  EARLIER APPLICATION NUMBER: PCT/JP97/03303
;  EARLIER FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 1026
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-068-880-14

  Query Match             11.6%;  Score 480;  DB 4;  Length 1026;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-220;
  Matches  480;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 TGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCT 60

Qy   3726 GCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAA 3785
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Db     61 GCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAA 120

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Qy   3846 ACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACA 3905
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Db    181 ACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACA 240

Qy   3906 AAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACC 3965
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Db    241 AAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACC 300

Qy   3966 ACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTAC 4025
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Db    301 ACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTGTGTAC 360

Qy   4026 AGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTG 4085
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCCACTTG 420

Qy   4086 GGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTTTAATC 4145
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Db    421 GGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTTTAATC 480

Search completed: March 14, 2003, 13:34:01

Job time : 154 secs
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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 08:01:33 ; Search time 10444 Seconds
(without alignments)
11550.281 Million cell updates/sec

Title: US-09-490-208-3
Perfect score: 4145
Sequence: 1 ctgctttaaaatctctcggc.....aattgcattttactttaatc 4145

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 50

Total number of hits satisfying chosen parameters: 92

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*
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2: gb_htg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4145	100.0	4145	6	I15516	I15516 Sequence 1
2	4145	100.0	4145	6	I61175	I61175 Sequence 1
3	4145	100.0	4145	9	HUMINOSA	L09210 Homo sapien
4	3503	84.5	35764	12	AY046510	AY046510 Adenovira
5	3482	84.0	4164	6	A39980	A39980 Sequence 1
6	3482	84.0	4164	9	HSINOSA	X73029 H.sapiens m
7	3381	81.6	4062	6	AR124185	AR124185 Sequence
8	3381	81.6	4062	9	HSU31511	U31511 Human induc
9	3357	81.0	4150	6	AX067222	AX067222 Sequence
10	3357	81.0	4150	9	AF068236	AF068236 Homo sapi
11	3327	80.3	3946	6	AX067221	AX067221 Sequence
12	3327	80.3	3946	9	HSU20141	U20141 Human induc
13	3290	79.4	3963	9	HUMITONOS	D26525 Human mRNA
14	3085	74.4	3595	9	HUMNOSIND	L24553 Homo sapien
15	3039	73.3	3855	9	HSU05810	U05810 Human induc
16	1970	47.5	3345	9	AB022318	AB022318 Homo sapi
17	585	14.1	604	6	AR142643	AR142643 Sequence
18	585	14.1	604	6	E28937	E28937 Method for
19	504	12.2	64641	2	AC130289	AC130289 Homo sapi
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c 21	504	12.2	156907	9	HS66C13	AL354047 Homo sapi
22	480	11.6	1026	6	AR142656	AR142656 Sequence
23	480	11.6	1026	6	E28948	E28948 Method for
24	286	6.9	634	9	HSNOS2E27	X85781 H.sapiens N
25	200	4.8	351	9	HSNOS2E12	X85768 H.sapiens N
c 26	197	4.8	64641	2	AC130289	AC130289 Homo sapi
c 27	185	4.5	174503	9	AC005697	AC005697 Homo sapi
28	183	4.4	268	9	HSNOS2E2	X85760 H.sapiens N
29	180	4.3	180	9	S76479	S76479 calcium-cal
30	179	4.3	339	9	HSNOS2E17	X85773 H.sapiens N
31	165	4.0	343	9	HSNOS2E6	X85764 H.sapiens N
c 32	155	3.7	343	9	HSU24641	U24641 Human chrom
33	155	3.7	566	9	HSNOS2X22	X81701 H.sapiens N
34	150	3.6	480	9	HSNOS2E11	X85767 H.sapiens N
35	147	3.5	348	9	HSNOS2E14	X85770 H.sapiens N
36	144	3.5	602	9	HSNOS2E89	X85766 H.sapiens N
37	137	3.3	269	9	HSNOS2E26	X85780 H.sapiens N
38	137	3.3	438	9	HSNOS2X25	X81702 H.sapiens N
39	135	3.3	273	9	HSNOS2E18	X85774 H.sapiens N
40	133	3.2	622	9	HUMIOXSYN	L26055 Human nitri
41	133	3.2	1291	9	HUMNOSB	D29675 Human induc
42	133	3.2	5493	9	HS5INOS	X97821 H.sapiens p
43	125	3.0	287	9	HSNOS2E5	X85763 H.sapiens N
44	110	2.7	1407	6	AX348110	AX348110 Sequence
45	110	2.7	8464	9	AF017634	AF017634 Homo sapi
46	107	2.6	285	9	HSNOS2E15	X85771 H.sapiens N
47	102	2.5	287	9	HSNOS2E7	X85765 H.sapiens N
48	99	2.4	490	9	MMU31907	U31907 Macaca mula
49	97	2.3	345	9	HSNOS2E21	X85777 H.sapiens N
50	96	2.3	918	9	HSNOS2E1	X85759 H.sapiens N
51	95	2.3	336	9	HSNOS2E20	X85776 H.sapiens N
52	88	2.1	208	9	HSNOS2E3	X85761 H.sapiens N
53	88	2.1	283	9	S75615	S75615 iNOS=nitric
54	86	2.1	445	4	AF254445	AF254445 Ovis arie
55	85	2.1	289	9	HSNOS2E13	X85769 H.sapiens N
56	84	2.0	152351	9	AC015688	AC015688 Homo sapi
c 57	84	2.0	186750	2	AC068106	AC068106 Homo sapi
58	81	2.0	293	9	HSNOS2E19	X85775 H.sapiens N
59	77	1.9	4050	4	AF077821	AF077821 Canis fam
60	63	1.5	247	9	HSNOS2E24	X85779 H.sapiens N
61	62	1.5	290	9	HSNOS2E23	X85778 H.sapiens N
62	61	1.5	3936	4	AY027883	AY027883 Equus cab
63	59	1.4	226	9	HSINOSX05	U65693 Human induc
64	59	1.4	310	4	AF469048	AF469048 Oryctolag
65	59	1.4	474	4	AF329377	AF329377 Equus cab

	66	56	1.4	278	9	HSNOS2E4	X85762 H.sapiens N
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c	71	53	1.3	126500	2	AC015885	AC015885 Homo sapi
	72	53	1.3	146243	2	AC130293	AC130293 Homo sapi
	73	53	1.3	158698	2	AC036181	AC036181 Homo sapi
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	80	53	1.3	208010	2	AC129927	AC129927 Homo sapi
	81	52	1.3	332	4	CHU29085	U29085 Capra hircu
	82	52	1.3	647	4	SSU59390	U59390 Sus scrofa
	83	52	1.3	1191	9	HSU50398	U50398 Human nitri
	84	52	1.3	3924	9	HSNITOSPR	Z49251 H.sapiens g
	85	50	1.2	290	4	OCU85093	U85093 Oryctolagus
c	86	50	1.2	130561	9	AC107983	AC107983 Homo sapi
	87	50	1.2	137007	2	AC090285	AC090285 Homo sapi
	88	50	1.2	162035	2	AC073519	AC073519 Homo sapi
c	89	50	1.2	169559	2	AC023401	AC023401 Homo sapi
c	90	50	1.2	175103	9	HS37N07	AL353997 Homo sapi
c	91	50	1.2	178078	2	AC127538	AC127538 Homo sapi
	92	50	1.2	194822	2	AC015818	AC015818 Homo sapi

ALIGNMENTS

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RESULT 1
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LOCUS       I15516                  4145 bp    DNA     linear   PAT 02-APR-1996
DEFINITION  Sequence 1 from patent US 5468630.
ACCESSION   I15516
VERSION     I15516.1  GI:1250424
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4145)
  AUTHORS   Billiar,T.R., Nussler,A.K., Geller,D.A. and Simmons,R.L.
  TITLE     cDNA clone for human inducible nitric oxide synthase and process
            for preparing same
  JOURNAL   Patent: US 5468630-A 1 21-NOV-1995;
FEATURES             Location/Qualifiers
     source          1. .4145
                     /organism="unknown"
BASE COUNT      968 a   1203 c   1126 g    848 t
ORIGIN

  Query Match           100.0%;  Score 4145;  DB 6;  Length 4145;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
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Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60

Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
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Db      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
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Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
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Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
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Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
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Db     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

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Db     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140

Qy    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
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Db  1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Qy  1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Db  1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
Qy  1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Db  1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
Qy  1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Db  1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
Qy  1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Db  1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
Qy  1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Db  1621 TCACCCCCGTGTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATC 1680
Qy  1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Db  1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
Qy  1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Db  1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
Qy  1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Db  1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
Qy  1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Db  1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
Qy  1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Db  1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
Qy  1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Db  1981 CGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGC 2040
Qy  2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Db  2041 TGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACC 2100
Qy  2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Db  2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
Qy  2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Db  2161 AGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCT 2220
Qy  2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Db  2221 GGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACA 2280
Qy  2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Db  2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
Qy  2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Db  2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
Qy  2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
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Db  2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
Qy  2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Db  2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
Qy  2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Db  2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
Qy  2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Db  2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
Qy  2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Db  2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
Qy  2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Db  2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
Qy  2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Db  2761 AAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGA 2820
Qy  2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Db  2821 AGTTCACCAACAGCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGT 2880
Qy  2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Db  2881 CTGCTGGCTTCCTGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCT 2940
Qy  2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Db  2941 CCTCCCGGGATCACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3000
Qy  3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Db  3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
Qy  3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Db  3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120
Qy  3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Db  3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180
Qy  3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Db  3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
Qy  3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
Db  3241 TGGTGTTTGGGTGCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGA 3300
Qy  3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
Db  3301 TGGCCCAGAAGGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGC 3360
Qy  3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
Db  3361 CCAAGGTCTATGTTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGC 3420
Qy  3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
Db  3421 TCCACAAGGAGCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGG 3480
Qy  3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
Db  3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540
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Qy   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTAT 3600

Qy   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3660

Qy   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3720

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Qy   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CTCAAGTCTTATTTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAA 3840

Qy   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTAGCACCCTGGATTGATCGGAGCCTCCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGG 3900

Qy   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 AGACAAAATCTTAAATGCCAGGCCTGGCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGT 3960

Qy   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GCACCACTTCAAGTGACCACCAGGAGGTGCTATCGCACCACTGTGTATTTAACTGCCTTG 4020

Qy   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080

Qy   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140

Qy   4141 TAATC 4145
          |||||
Db   4141 TAATC 4145
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RESULT 2
I61175
LOCUS       I61175                  4145 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5658565.
ACCESSION   I61175
VERSION     I61175.1  GI:2479123
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4145)
  AUTHORS   Billiar,T.R., Tzeng,E., Nussler,A.K., Geller,D.A. and Simmons,R.L.
  TITLE     Inducible nitric oxide synthase gene for treatment of disease
  JOURNAL   Patent: US 5658565-A 1 19-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .4145
                     /organism="unknown"
BASE COUNT      968 a   1203 c   1126 g    848 t
ORIGIN

  Query Match             100.0%;  Score 4145;  DB 6;  Length 4145;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
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Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240

Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300

Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
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Db    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
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Db    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960

Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020

Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
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Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320

Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
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Db    4141 TAATC 4145
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RESULT 3
HUMINOSA
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DEFINITION  Homo sapiens inducible nitric oxide synthase mRNA, complete cds.
ACCESSION   L09210
VERSION     L09210.1  GI:292241
KEYWORDS    inducible gene; nitric oxide synthase.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4145)
  AUTHORS   Geller,D.A., Lowenstein,C.J., Shapiro,R.A., Nussler,A.K., Di
            Silvio,M., Wang,S.C., Nakayama,D.K., Simmons,R.L., Snyder,S.H. and
            Billiar,T.R.
  TITLE     Molecular cloning and expression of inducible nitric oxide synthase
            from human hepatocytes
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (8), 3491-3495 (1993)
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ORIGIN
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ACCESSION   AY046510
VERSION     AY046510.1  GI:15636799
KEYWORDS    .
SOURCE      Adenoviral expression vector Ad-hiNOS.
  ORGANISM  Adenoviral expression vector Ad-hiNOS
            artificial sequences; vectors.
REFERENCE   1  (bases 1 to 35764)
  AUTHORS   Shapiro,R., Gao,W., Tzeng,E., Robbins,P.D., Timoty,B.R. and
            Gambotto,A.
  TITLE     Construction and characterization of a clinical grade adenoviral
            vector encoding the human iNOS cDNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 35764)
  AUTHORS   Shapiro,R., Gao,W., Tzeng,E., Robbins,P.D., Timoty,B.R. and
            Gambotto,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUL-2001) Surgery, University of Pittsburgh, 300
            Technology Drive, Pittsburgh, PA 15219, USA
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Matches 3503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   2367 AGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCATGAGGCTCAAATCTCGG 2426
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DEFINITION  Sequence 1 from Patent WO9423038.
ACCESSION   A39980
VERSION     A39980.1  GI:2296175
KEYWORDS    .
SOURCE      Homo sapiens.
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REFERENCE   1  (bases 1 to 4164)
  AUTHORS   Moncada,S.E., Charles,I.G. and Palmer,R.M.
  TITLE     INDUCIBLE NITRIC OXIDE SYNTHASE AND GENE THEREFOR
  JOURNAL   Patent: WO 9423038-A 1 13-OCT-1994;
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COMMENT     Other publication AU 6287894 941024.
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BASE COUNT      974 a   1210 c   1127 g    853 t
ORIGIN

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Qy    1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
Db    1340 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1399

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Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
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Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060
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Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240
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Qy    4021 TGTACAGTTATTTATGCCTCTGTATTTAAAAAACTAACACCCAGTCTGTTCCCCATGGCC 4080
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Qy    4081 ACTTGGGTCTTCCCTGTATGATTCCTTGATGGAGATATTTACATGAATTGCATTTTACTT 4140
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Qy    4141 TAATC 4145
Db    4160 TAATC 4164
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RESULT 6
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DEFINITION  H.sapiens mRNA for nitric oxide synthase.
ACCESSION   X73029
VERSION     X73029.1  GI:441452
KEYWORDS    nitric oxide synthase.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4164)
  AUTHORS   Charles,I.G., Palmer,R.M., Hickery,M.S., Bayliss,M.T., Chubb,A.P.,
            Hall,V.S., Moss,D.W. and Moncada,S.
  TITLE     Cloning, characterization, and expression of a cDNA encoding an
            inducible nitric oxide synthase from the human chondrocyte
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (23), 11419-11423 (1993)
  MEDLINE   94068614
   PUBMED   7504305
REFERENCE   2  (bases 1 to 4164)
  AUTHORS   Charles,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-APR-1993) I. Charles, Wellcome Research Laboratories,
            Ble. 113, Deot. of Cekk Biology, Langley Park, Beckenham, Kent, BR3
            3BS, UK
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ORIGIN
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Qy      61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
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Qy     121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
Db     140 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 199

Qy     181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
Db     200 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 259

Qy     241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
Db     260 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 319

Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
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Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
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Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
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Qy     601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
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Db    680 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 739

Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
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Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
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Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
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Db    860 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 919

Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
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Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
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Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
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Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
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Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
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Db   2960 CCTCCCGGGATCACACGCCCACAGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACA 3019

Qy   3001 CCGGAGATGGCCAGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGA 3060

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Qy   3061 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGG 3120

Db   3080 AGCCCCAAGACCCAGTGCCCTGCTTTGTGCGGAATGCCAGCGGCTTCCACCTCCCCGAGG 3139

Qy   3121 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTT 3180

Db   3140 ATCCCTCCCATCCTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCAGTT 3199

Qy   3181 TCTGGCAGCAACGGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCT 3240

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Qy   3481 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3540

Db   3500 CCCACACCCTGAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGG 3559

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Db   3560 ACTATTTCTTTCAGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTTGGTGCTGTAT 3619

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Db   3620 TTCCTTACGAGGCGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAG 3679

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Db   3680 CGCTCTGAGGGCCTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCA 3739

Qy   3721 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3780

Db   3740 GCTCTGCATTATCTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGC 3799

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Qy   4141 TAATC 4145

Db   4160 TAATC 4164
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RESULT 7
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LOCUS       AR124185               4062 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 11 from patent US 6171856.
ACCESSION   AR124185
VERSION     AR124185.1  GI:14109546
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4062)
  AUTHORS   Thigpen,A., Hohmeier,H.-E., Newgard,C.B., Unger,R.H.,
            Shimabukuro,M., Chen,G., Rhodes,C.J., Hugl,S.R. and Cousin,S.
  TITLE     Methods and compositions relating to no-mediated cytotoxicity
  JOURNAL   Patent: US 6171856-A 11 09-JAN-2001;
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 4031; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy    462 AGGATCAAAAACTGGGGCAGCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAA 521

Db    361 AGGATCAAAAACTGGGGCAGCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAA 420

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Qy    642 TTTGTCAACCAATATTACGGCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGG 701
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Qy   1122 CCCCTGGTCCTGCAGGCCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTT 1181
Db   1021 CCCCTGGTCCTGCAGGCCAATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTT 1080
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Db   1141 TGGTACGCCCTGCCTGCAGTGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCA 1200
Qy   1302 GGGTGCCCCTTCAATGGCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGAC 1361
Db   1201 GGGTGCCCCTTCAATGGCTGGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGAC 1260
Qy   1362 GTCCAGCGCTACAACATCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAG 1421
Db   1261 GTCCAGCGCTACAACATCCTGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAG 1320
Qy   1422 CTGGCCTCGCTCTGGAAAGACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGT 1481
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Qy   1482 TTTCAGAAGCAGAATGTGACCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAG 1541
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Qy   1542 TACATGCAGAATGAATACCGGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTC 1601
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Qy   1842 GAGACAGGAAAATCAGAGGCGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTC 1901
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Qy   1902 AACCCCAAGGTTGTCTGCATGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTG 1961
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Qy   1962 CTGTTGGTGGTGACCAGTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTG 2021
Db   1861 CTGTTGGTGGTGACCAGTACGTTTGGCAATGGAGACTGCCCTGGCAATGGAGAGAAACTG 1920
Qy   2022 AAGAAATCGCTCTTCATGCTGAAAGAGCTCAACAACAAATTCAGGTACGCTGTGTTTGGC 2081
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Qy   2082 CTCGGCTCCAGCATGTACCCTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTG 2141
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Qy   2142 TCCCACCTGGGGGCCTCTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAG 2201
Db   2041 TCCCACCTGGGGGCCTCTCAGCTCACCCCGATGGGAGAAGGGGATGAGCTCAGTGGGCAG 2100
Qy   2202 GAGGACGCCTTCCGCAGCTGGGCCGTGCAAACCTTCAAGGCAGCCTGTGAGACGTTTGAT 2261
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Qy   2262 GTCCGAGGCAAACAGCACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGAC 2321
Db   2161 GTCCGAGGCAAACAGCACATTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGAC 2220
Qy   2322 CCGCACCACTACAGGCTCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGC 2381
Db   2221 CCGCACCACTACAGGCTCGTGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGC 2280
Qy   2382 AGCATGCATGCCAAGAACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGT 2441
Db   2281 AGCATGCATGCCAAGAACGTGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGT 2340
Qy   2442 CCGACATCCAGCCGTGCCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTG 2501
Db   2341 CCGACATCCAGCCGTGCCACCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTG 2400
Qy   2502 AACTACCTGCCGGGGGAGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAA 2561
Db   2401 AACTACCTGCCGGGGGAGCACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAA 2460
Qy   2562 GGCATCCTGGAGCGAGTGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGAC 2621
Db   2461 GGCATCCTGGAGCGAGTGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCC 2520
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Qy   2682 CAGGCCCTCACCTACTCCCCGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAG 2741
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Qy   2742 CTGGCCCAGGTGGCCACAGAAGAGCCTGAGAGACAGAGGCTGGAGGCCCTGTGCCAGCCC 2801
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DEFINITION  Human inducible nitric oxide synthase (NOS) mRNA, complete cds.
ACCESSION   U31511
VERSION     U31511.1  GI:951320
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 4062)
  AUTHORS   Park,C.S., Park,R. and Krishna,G.
  TITLE     Constitutive expression and structural diversity of inducible
            isoform of nitric oxide synthase in human tissues
  JOURNAL   Life Sci. 59 (3), 219-225 (1996)
  MEDLINE   96276472
   PUBMED   8699932
REFERENCE   2  (bases 1 to 4062)
  AUTHORS   Park,C., Gianotti,C., Park,R. and Krishna,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1995) Chang-Shin Park, Lab. of Molecular
            Immunology, NHLBI, 9000 Rockville Pike, Bethesda, MD 20892-1760,
            USA
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Qy    102 TACCCCGGGGAGGCAGTGCAGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAA 161
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Qy    162 ATCCAGATAAGTGACATAAGTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGG 221
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Qy    402 AAGTCTCCAGAATCTCTGGTCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTG 461
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Qy    582 ACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAA 641
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Qy    702 GTGGAAGCGGTAACAAAGGAGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAG 761
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Qy    822 TGGTCCAACCTGCAGGTCTTCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAA 881
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Qy    942 GTGTTCCCCCAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATC 1001
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Qy   1002 CGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAA 1061
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Qy   2562 GGCATCCTGGAGCGAGTGGTGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGAC 2621
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Db   4021 CATGAATTGCATTTTACTTTAATC 4044


RESULT 9
AX067222
LOCUS       AX067222               4150 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 3 from Patent WO0078946.
ACCESSION   AX067222
VERSION     AX067222.1  GI:12544879
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4150)
  AUTHORS   Keller,E.T., Gravenstein,S. and Hall,D.M.
  TITLE     Treatment of viral influenza with antisense oligonucleotides
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            Eastern Virginia Medical School (US)
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Qy     301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
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Qy     361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
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Qy     421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
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Qy     481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
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Qy     541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
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Qy     661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
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Db    1709 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1768
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Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
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Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
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Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
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Db   2609 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCT 2668

Qy   2641 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCC 2700
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Db   2669 ACTGGGTCAGTGACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTTCC 2728

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RESULT 10
AF068236
LOCUS       AF068236               4150 bp    mRNA    linear   PRI 07-JUN-1998
DEFINITION  Homo sapiens inducible nitric oxide synthase (NOS) mRNA, complete
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ACCESSION   AF068236
VERSION     AF068236.1  GI:3192916
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4150)
  AUTHORS   Luss,H., Li,R.-K., Shapiro,R.A., Tzeng,E., McGowan,F.X.,
            Yoneyama,T., Hatakayama,K., Geller,D.A., Mickle,D.A.G.,
            Simmons,R.L. and Billiar,T.R.
  TITLE     Dedifferentiated human ventricular cardiac myocytes express
            inducible nitric oxide synthase mRNA but not protein in response to
            IL-1, TNF, IFNgamma, and LPS
  JOURNAL   J. Mol. Cell. Cardiol. 29 (4), 1153-1165 (1997)
  MEDLINE   97304504
   PUBMED   9160867
REFERENCE   2  (bases 1 to 4150)
  AUTHORS   Luss,H., Li,R.-K., Shapiro,R.A., Tzeng,E., McGowan,F.X.,
            Yoneyama,T., Hatakayama,K., Geller,D.A., Mickle,D.A.G.,
            Simmons,R.L. and Billiar,T.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAY-1998) Pharmacology, Westf.Wilhelms-Univ.,
            Domagkstr. 12, Munster D-48149, Germany
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                     QTVRLEALDESGSYWVSDKRLPPCSLSQALTYFLDITTPPTQLLLQKLAQVATEEPER
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ORIGIN
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Qy      1 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 60
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Db     29 CTGCTTTAAAATCTCTCGGCCACCTTTGATGAGGGGACTGGGCAGTTCTAGACAGTCCCG 88

Qy     61 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89 AAGTTCTCAAGGCACAGGTCTCTTCCTGGTTTGACTGTCCTTACCCCGGGGAGGCAGTGC 148

Qy    121 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    149 AGCCAGCTGCAAGCCCCACAGTGAAGAACATCTGAGCTCAAATCCAGATAAGTGACATAA 208

Qy    181 GTGACCTGCTTTGTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCA 240
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Qy    241 AATTCCACCAGTATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    301 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    329 CCTGTGCCACCTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGC 388

Qy    361 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 420
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Db    389 AGCAGAATGAGTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGG 448

Qy    421 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    449 TCAAGCTGGATGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCA 508

Qy    481 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    509 GCGGGATGACTTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGT 568

Qy    541 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 600
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Db    569 CCAAATCTTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACA 628

Qy    601 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 660
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Db    629 AGCCTACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACG 688

Qy    661 GCTCCTTCAAAGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGG 720
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Qy    721 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 780
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Db    749 AGATAGAAACAACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGC 808

Qy    781 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 840
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Db    809 AGGCCTGGCGCAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCT 868

Qy    841 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 900
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Db    869 TCGATGCCCGCAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGC 928
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Qy    901 GTTACTCCACCAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTG 960
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Qy    961 ATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGA 1020
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Qy   1021 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1080
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Db   1049 TGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCG 1108

Qy   1081 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1140
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Db   1109 ACCTGGGCTGGAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCA 1168

Qy   1141 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1169 ATGGCCGTGACCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGG 1228

Qy   1201 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1260
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Db   1229 AACATCCCAAATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAG 1288

Qy   1261 TGGCCAACATGCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCT 1320
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Qy   1321 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1380
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Db   1349 GGTACATGGGCACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCC 1408

Qy   1381 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1440
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Db   1409 TGGAGGAAGTGGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAG 1468

Qy   1441 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGA 1500
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Db   1469 ACCAGGCTGTCGTTGAGATCAACATTGCTGTGCTCCATAGTTTTCAGAAGCAGAATGTGA 1528

Qy   1501 CCATCATGGACCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACC 1560
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Qy   1561 GGTCCCGTGGGGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCA 1620
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Qy   1681 AGGTAGAGGCCTGGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAG 1740
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Qy   1741 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1800
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Db   1769 AGATTCCATTGAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGA 1828

Qy   1801 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGG 1860
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Db   1829 CAATGGCGTCCCGAGTCAGAGTCACCATCCTCTTTGCTACAGAGACAGGAAAATCAGAGG 1888

Qy   1861 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1920
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Db   1889 CGCTGGCCTGGGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCA 1948

Qy   1921 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 1980
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Db   1949 TGGATAAGTACAGGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTA 2008

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Qy   2101 CTCGGTTCTGCGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTC 2160
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Qy   2281 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2340
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Db   2309 TTCAGATCCCCAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCG 2368

Qy   2341 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2400
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Db   2369 TGCAGGACTCACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACG 2428

Qy   2401 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2460
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Db   2429 TGTTCACCATGAGGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCA 2488

Qy   2461 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2520
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Db   2489 CCATCCTGGTGGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGC 2548

Qy   2521 ACCTTGGGGTTTGCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGG 2580
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Qy   2581 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCT 2640
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Db   2609 TGGATGGCCCCACACCCCACCAGACAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCT 2668

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Qy   2701 CGGACATCACCACACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAG 2760
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RESULT 11
AX067221

LOCUS       AX067221               3946 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 2 from Patent WO0078946.
ACCESSION   AX067221
VERSION     AX067221.1  GI:12544878
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3946)
  AUTHORS   Keller,E.T., Gravenstein,S. and Hall,D.M.
  TITLE     Treatment of viral influenza with antisense oligonucleotides
  JOURNAL   Patent: WO 0078946-A 2 28-DEC-2000;
            Eastern Virginia Medical School (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
BASE COUNT      918 a   1149 c   1073 g    806 t
ORIGIN

  Query Match             80.3%;  Score 3327;  DB 6;  Length 3946;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 3927;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

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Db      1 ATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCAGTATGCAATGAATGGG 60

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Db     61 GAAAAAGACATCAACAACAATGTGGAGAAAGCCCCCTGTGCCACCTCCAGTCCAGTGACA 120

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Qy    387 GTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGATGCAACCCCATTGTCC 446
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Qy    447 TCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGACTTTCCAAGACACACTT 506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    507 CACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTGCCTGGGGTCCATTATG 566
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Qy    567 ACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTA 626
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Qy    687 GAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAACAACAGGAACCTACCAA 746
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Qy    747 CTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCAATGCCCCACGCTGC 806
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Db    541 CTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCAATGCCCCACGCTGC 600

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Qy    867 CGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCACCAACAATGGCAACATC 926
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Qy   1587 TGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGTGTTTCACCAGGAGATG 1646
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Qy   1647 CTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGCCTGGAAAACCCATGTC 1706
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Qy   2547 CCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGGTGGATGGCCCCACACCCCACCAGACA 2606
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RESULT 12
HSU20141

LOCUS       HSU20141                3946 bp    mRNA    linear   PRI 12-AUG-1995
DEFINITION  Human inducible nitric oxide synthase mRNA, complete cds.
ACCESSION   U20141
VERSION     U20141.1  GI:687680
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3946)
  AUTHORS   Guo,F.H., De Raeve,H.R., Rice,T.W., Stuehr,D.J., Thunnissen,F.B.
            and Erzurum,S.C.
  TITLE     Continuous nitric oxide synthesis by inducible nitric oxide
            synthase in normal human airway epithelium in vivo
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 92 (17), 7809-7813 (1995)
  MEDLINE   95372368
   PUBMED   7544004
REFERENCE   2  (bases 1 to 3946)
  AUTHORS   Erzurum,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JAN-1995) Serpil C. Erzurum, Pulmonary & Critical
            Care Medicine, Cleveland Clinic Foundation, 9500 Euclid Avenue,
            Cleveland, OH 44195, USA
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     polyA_site      3946
BASE COUNT      918 a   1149 c   1073 g    806 t
ORIGIN

  Query Match             80.3%;  Score 3327;  DB 9;  Length 3946;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 3927;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy     207 ATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCAGTATGCAATGAATGGG 266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCAGTATGCAATGAATGGG 60

Qy     267 GAAAAAGACATCAACAACAATGTGGAGAAAGCCCCCTGTGCCACCTCCAGTCCAGTGACA 326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      61 GAAAAAGACATCAACAACAATGTGGAGAAAGCCCCCTGTGCCACCTCCAGTCCAGTGACA 120

Qy     327 CAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGAGTCCCCGCAGCCCCTC 386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGAGTCCCCGCAGCCCCTC 180

Qy     387 GTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGATGCAACCCCATTGTCC 446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGATGCAACCCCATTGTCC 240

Qy     447 TCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGACTTTCCAAGACACACTT 506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGACTTTCCAAGACACACTT 300

Qy     507 CACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTGCCTGGGGTCCATTATG 566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTGCCTGGGGTCCATTATG 360

Qy     567 ACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTA 626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTCCAGATGAGCTTCTA 420

Qy     627 CCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCTTCAAAGAGGCAAAAATAGAG 686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCTTCAAAGAGGCAAAAATAGAG 480

Qy     687 GAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAACAACAGGAACCTACCAA 746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAACAACAGGAACCTACCAA 540

Qy     747 CTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCAATGCCCCACGCTGC 806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCAATGCCCCACGCTGC 600

Qy     807 ATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCGCAGCTGTTCCACTGCC 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCGCAGCTGTTCCACTGCC 660

Qy     867 CGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCACCAACAATGGCAACATC 926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCACCAACAATGGCAACATC 720

Qy     927 AGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGG 986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGG 780

Qy     987 AATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGAC 1046
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Db     781 AATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGAC 840

Qy    1047 CCTGCCAACGTGGAATTCACTCAGCTGTGCATCGACCTGGGCTGGAAGCCCAAGTACGGC 1106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTGCCAACGTGGAATTCACTCAGCTGTGCATCGACCTGGGCTGGAAGCCCAAGTACGGC 900

Qy    1107 CGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGACCCTGAGCTCTTCGAA 1166
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Db     901 CGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGACCCTGAGCTCTTCGAA 960

Qy    1167 ATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAAATACGAGTGGTTTCGG 1226
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Db     961 ATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAAATACGAGTGGTTTCGG 1020

Qy    1227 GAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACATGCTGCTTGAGGTGGGC 1286
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Db    1021 GAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACATGCTGCTTGAGGTGGGC 1080

Qy    1287 GGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGGCACAGAGATCGGAGTC 1346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGGCACAGAGATCGGAGTC 1140

Qy    1347 CGGGACTTCTGTGACGTCCAGCGCTACAACATCCTGGAGGAAGTGGGCAGGAGAATGGGC 1406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGGGACTTCTGTGACGTCCAGCGCTACAACATCCTGGAGGAAGTGGGCAGGAGAATGGGC 1200

Qy    1407 CTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGTCGTTGAGATCAACATT 1466
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Db    1201 CTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGTCGTTGAGATCAACATT 1260

Qy    1467 GCTGTGATCCATAGTTTTCAGAAGCAGAATGTGACCATCATGGACCACCACTCGGCTGCA 1526
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Db    1261 GCTGTGCTCCATAGTTTCCAGAAGCAGAATGTGACCATCATGGACCACCACTCGGCTGCA 1320

Qy    1527 GAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGGGGGCTGCCCGGCAGAC 1586
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Db    1321 GAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGGGGGCTGCCCGGCAGAC 1380

Qy    1587 TGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGTGTTTCACCAGGAGATG 1646
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Db    1381 TGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGTGTTTCACCAGGAGATG 1440

Qy    1647 CTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGCCTGGAAAACCCATGTC 1706
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGCCTGGAAAACCCATGTC 1500

Qy    1707 TGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAGAGATTCCATTGAAAGTCTTGGTCAAA 1766
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAGAGATTCCATTGAAAGTCTTGGTCAAA 1560

Qy    1767 GCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGACAATGGCGTCCCGAGTCAGAGTCACC 1826
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGACAATGGCGTCCCGAGTCAGAGTCACC 1620

Qy    1827 ATCCTCTTTGCGACAGAGACAGGAAAATCAGAGGCGCTGGCCTGGGACCTGGGGGCCTTA 1886
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 ATCCTCTTTGCGACAGAGACAGGAAAATCAGAGGCGCTGGCCTGGGACCTGGGGGCCTTA 1680

Qy    1887 TTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCATGGATAAGTACAGGCTGAGCTGCCTG 1946
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 TTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCATGGATAAGTACAGGCTGAGCTGCCTG 1740

Qy    1947 GAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTACGTTTGGCAATGGAGACTGCCCTGGC 2006
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTACGTTTGGCAATGGAGACTGCCCTGGC 1800

Qy    2007 AATGGAGAGAAACTGAAGAAATCGCTCTTCATGCTGAAAGAGCTCAACAACAAATTCAGG 2066
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AATGGAGAGAAACTGAAGAAATCGCTCTTCATGCTGAAAGAGCTCAACAACAAATTCAGG 1860

Qy    2067 TACGCTGTGTTTGGCCTCGGCTCCAGCATGTACCCTCGGTTCTGCGCCTTTGCTCATGAC 2126
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Db    1861 TACGCTGTGTTTGGCCTCGGCTCCAGCATGTACCCTCGGTTCTGTGCCTTTGCTCATGAC 1920

Qy    2127 ATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTCAGCTCACCCCGATGGGAGAAGGGGAT 2186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTCAGCTCACCCCGATGGGAGAAGGGGAT 1980

Qy    2187 GAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCTGGGCCGTGCAAACCTTCAAGGCAGCC 2246
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Qy    2247 TGTGAGACGTTTGATGTCCGAGGCAAACAGCACATTCAGATCCCCAAGCTCTACACCTCC 2306
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Db    2041 TGTGAGACGTTTGATGTCCGAGGCAAACAGCACATTCAGATCCCCAAGCTCTACACCTCC 2100

Qy    2307 AATGTGACCTGGGACCCGCACCACTACAGGCTCGTGCAGGACTCACAGCCTTTGGACCTC 2366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 AATGTGACCTGGGACCCGCACCACTACAGGCTCGTGCAGGACTCACAGCCTTTGGACCTC 2160

Qy    2367 AGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCATGAGGCTCAAATCTCGG 2426
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 AGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCATGAGGCTCAAATCTCGG 2220

Qy    2427 CAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGTGGAACTCTCCTGTGAG 2486
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Db    2221 CAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGTGGAACTCTCCTGTGAG 2280
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Qy   2487 GATGGCCAAGGCCTGAACTACCTGCCGGGGGAGCACCTTGGGGTTTGCCCAGGCAACCAG 2546
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Db   2281 GATGGCCAAGGCCTGAACTACCTGCCGGGGGAGCACCTTGGGGTTTGCCCAGGCAACCAG 2340

Qy   2547 CCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGGTGGATGGCCCCACACCCCACCAGACA 2606
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCGGCCCTGGTCCAAGGTATCCTGGAGCGAGTGGTGGATGGCCCCACACCCCACCAGACA 2400

Qy   2607 GTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCTACTGGGTCAGTGACAAGAGGCTGCCC 2666
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCTACTGGGTCAGTGACAAGAGGCTGCCC 2460

Qy   2667 CCCTGCTCACTCAGCCAGGCCCTCACCTACTCCCCGGACATCACCACACCCCCAACCCAG 2726
          |||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Db   2461 CCCTGCTCACTCAGCCAGGCCCTCACCTACTTCCTGGACATCACCACACCCCCAACCCAG 2520

Qy   2727 CTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAGAAGAGCCTGAGAGACAGAGGCTGGAG 2786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2787 GCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGAAGTTCACCAACAGCCCCACATTCCTG 2846
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Qy   2847 GAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGTCTGCTGGCTTCCTGCTTTCCCAGCTC 2906
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Qy   2907 CCCATTCTGAAGCCCAGGTTCTACTCCATCAGCTCCTCCCGGGATCACACGCCCACGGAG 2966
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Db   2701 CCCATTCTGAAGCCCAGGTTCTACTCCATCAGCTCCTCCCGGGATCACACGCCCACAGAG 2760

Qy   2967 ATCCACCTGACTGTGGCCGTGGTCACCTACCACACCGGAGATGGCCAGGGTCCCCTGCAC 3026
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Qy   3027 CACGGTGTCTGCAGCACATGGCTCAACAGCCTGAAGCCCCAAGACCCAGTGCCCTGCTTT 3086
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Db   2821 CACGGTGTCTGCAGCACATGGCTCAACAGCCTGAAGCCCCAAGACCCAGTGCCCTGCTTT 2880

Qy   3087 GTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGGATCCCTCCCATCCTTGCATCCTCATC 3146
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Qy   3147 GGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTTTCTGGCAGCAACGGCTCCATGACTCC 3206
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Db   2941 GGGCCTGGCACAGGCATCGCGCCCTTCCGCAGTTTCTGGCAGCAACGGCTCCATGACTCC 3000

Qy   3207 CAGCACAAGGGAGTGCGGGGAGGCCGCATGACCTTGGTGTTTGGGTGCCGCCGCCCAGAT 3266
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Db   3001 CAGCACAAGGGAGTGCGGGGAGGCCGCATGACCTTGGTGTTTGGGTGCCGCCGCCCAGAT 3060

Qy   3267 GAGGACCACATCTACCAGGAGGAGATGCTGGAGATGGCCCAGAAGGGGGTGCTGCATGCG 3326
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Qy   3327 GTGCACACAGCCTATTCCCGCCTGCCTGGCAAGCCCAAGGTCTATGTTCAGGACATCCTG 3386
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Db   3121 GTGCACACAGCCTATTCCCGCCTGCCTGGCAAGCCCAAGGTCTATGTTCAGGACATCCTG 3180

Qy   3387 CGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGCTCCACAAGGAGCCAGGCCACCTCTAT 3446
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Db   3181 CGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGCTCCACAAGGAGCCAGGCCACCTCTAT 3240

Qy   3447 GTTTGCGGGGATGTGCGCATGGCCCGGGACGTGGCCCACACCCTGAAGCAGCTGGTGGCT 3506
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Qy   3507 GCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGGACTATTTCTTTCAGCTCAAGAGCCAG 3566
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Qy   3627 GTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAGCGCTCTGAGGGCCTACAGGAGGGGTT 3686
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Qy   3687 AAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTATCTGAGGTCACAGGG 3746
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Qy   3747 CCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTATTTCCTCAACGTTGC 3806
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Qy   3807 TCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGGATTGATCGGAGCCT 3866
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Qy   3867 CCTCTCTCAAACTGGGGCCTCCCTGGTCCCTTGGAGACAAAATCTTAAATGCCAGGCCTG 3926
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Qy   3927 GCGAGTGGGTGAAAGATGGAACTTGCTGCTGAGTGCACCACTTCAAGTGACCACCAGGAG 3986
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RESULT 13
HUMITONOS
LOCUS       HUMITONOS               3963 bp    mRNA    linear   PRI 04-OCT-2001
DEFINITION  Human mRNA for inducible type of nitric oxide synthase, complete
            cds.
ACCESSION   D26525
VERSION     D26525.1  GI:559326
KEYWORDS    inducible type of nitric oxide synthase; cytokine-related.
SOURCE      Homo sapiens glioblastoma cell_line:A-172 cDNA to mRNA,
            clone_lib:lambda ZAPII.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3963)
  AUTHORS   Hokari,A., Zeniya,M. and Esumi,H.
  TITLE     Cloning and functional expression of human inducible nitric oxide
            synthase (NOS) cDNA from a glioblastoma cell line A-172
  JOURNAL   J. Biochem. 116 (3), 575-581 (1994)
  MEDLINE   95155267
REFERENCE   2  (bases 1 to 3963)
  AUTHORS   Hokari,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JAN-1994) Atsushi Hokari, Jikei University School of
            Medicine, Tokyo, Department of Internal medicine, Division of
            Gastroenterology and Hepatology; 3-25-8 Nishishimbashi, Minato,
            Tokyo 105-0003, Japan (E-mail:hokari_a@jikei.ac.jp,
            Tel:03-3433-1111, Fax:03-3435-0569)
FEATURES             Location/Qualifiers
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                     /cell_line="A-172"
                     /tissue_type="glioblastoma"
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                     recognition sites for the cofactors FMN, FAD and NADPH and
                     calmodulin recognition sites."
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                     /product="inducible type of nitric oxide synthase"
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                     PKVVCMDKYRLSCLEEERLLLVVTSTFGNGDCPGNGEKLKKLLFMLKELNNKFRYAVF
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                     SLEMSAL"
BASE COUNT      930 a    1152 c    1077 g     804 t
ORIGIN

  Query Match             79.4%;  Score 3290;  DB 9;  Length 3963;
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  Matches 3940;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy     193 GTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCAGT 252
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Qy     253 ATGCAATGAATGGGGAAAAAGACATCAACAACAATGTGGAGAAAGCCCCCTGTGCCACCT 312
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Qy     313 CCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGAGT 372
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Qy     373 CCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGATG 432
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Db     181 CCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGATG 240

Qy     433 CAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGACTT 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     493 TCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTGCC 552
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Qy     553 TGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTC 612
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Db     361 TGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCCTC 420

Qy     613 CAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCTTCAAAG 672
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Qy     733 CAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCGCA 792
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Qy     853 GCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCACCA 912
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Qy     973 ACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCA 1032
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Qy    1093 AGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGACC 1152
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Db     901 AGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGACC 960

Qy    1153 CTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAAAT 1212
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Qy    1213 ACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACATGC 1272
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Qy    1273 TGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGGCA 1332
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Qy    1333 CAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCCTGGAGGAAGTGG 1392
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Qy    1393 GCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGTCG 1452
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Qy    1453 TTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGACCATCATGGACC 1512
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Qy    1513 ACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGGGG 1572
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Db    1321 ACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGGGG 1380

Qy    1573 GCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGTGT 1632
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Qy    1633 TTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGCCT 1692
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Qy    1693 GGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAGAGATTCCATTGA 1752
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Qy    1753 AAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGACAATGGCGTCCC 1812
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Qy   1813 GAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGGCGCTGGCCTGGG 1872
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Qy   1933 GGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTACGTTTGGCAATG 1992
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Db   1741 GGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTACGTTTGGCAATG 1800

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Db   1921 CCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTCAGCTCACCCCGA 1980

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Qy   2353 AGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCATGA 2412
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Qy   2413 GGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGTGG 2472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGTGG 2280

Qy   2473 AACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGGAGCACCTTGGGGTTT 2532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGGAGCACCTTGGGGTTT 2340

Qy   2533 GCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGGTGGATGGCCCCA 2592
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RESULT 14
HUMNOSIND
LOCUS       HUMNOSIND               3595 bp    mRNA    linear   PRI 30-SEP-1993
DEFINITION  Homo sapiens inducible nitric oxide synthase mRNA, complete cds.
ACCESSION   L24553
VERSION     L24553.1  GI:404048
KEYWORDS    nitric oxide synthase.
SOURCE      Homo sapiens (library: ATCC ccl221) colorectal adenocarcinoma cDNA
            to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3595)
  AUTHORS   Sherman,P.A., Laubach,V.E., Reep,B.R. and Wood,E.R.
  TITLE     Purification and cDNA sequence of an inducible nitric oxide
            synthase from a human tumour cell line
  JOURNAL   Biochemistry (1993) In press
FEATURES             Location/Qualifiers
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ORIGIN

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Db     181 CTCCAGTCCAGTGACACAGGATGACCTTCAGTATCACAACCTCAGCAAGCAGCAGAATGA 240

Qy     371 GTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGA 430
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Db     241 GTCCCCGCAGCCCCTCGTGGAGACGGGAAAGAAGTCTCCAGAATCTCTGGTCAAGCTGGA 300

Qy     431 TGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGAC 490
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TGCAACCCCATTGTCCTCCCCACGGCATGTGAGGATCAAAAACTGGGGCAGCGGGATGAC 360

Qy     491 TTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTG 550
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TTTCCAAGACACACTTCACCATAAGGCCAAAGGGATTTTAACTTGCAGGTCCAAATCTTG 420

Qy     551 CCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCC 610
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Db     421 CCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCCTACCCC 480

Qy     611 TCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCTTCAA 670
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTCAACCAATATTACGGCTCCTTCAA 540

Qy     671 AGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAAC 730
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AGAGGCAAAAATAGAGGAACATCTGGCCAGGGTGGAAGCGGTAACAAAGGAGATAGAAAC 600

Qy     731 AACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCG 790
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AACAGGAACCTACCAACTGACGGGAGATGAGCTCATCTTCGCCACCAAGCAGGCCTGGCG 660

Qy     791 CAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCG 850
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CAATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCG 720

Qy     851 CAGCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCAC 910
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Db     781 CAACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCA 840

Qy     971 CGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGG 1030
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Db     841 CGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGG 900

Qy    1031 CAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCGACCTGGGCTG 1090
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Qy    1091 GAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGA 1150
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Db     961 GAAGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGA 1020

Qy    1151 CCCTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAA 1210
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Db    1081 ATACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACAT 1140

Qy    1271 GCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGG 1330
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Db  1141 GCTGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGG 1200
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Db  1201 CACAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCCTGGAGGAAGT 1260
Qy  1391 GGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGT 1450
Db  1261 GGGCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGT 1320
Qy  1451 CGTTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGACCATCATGGA 1510
Db  1321 CGTTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATGTGACCATCATGGA 1380
Qy  1511 CCACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGG 1570
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Qy  1571 GGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGT 1630
Db  1441 GGGCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGT 1500
Qy  1631 GTTTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGC 1690
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Qy  1751 GAAAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGACAATGGCGTC 1810
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Qy  1811 CCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGGCGCTGGCCTG 1870
Db  1681 CCGAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGGCGCTGGCCTG 1740
Qy  1871 GGACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCATGGATAAGTA 1930
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Qy  1991 TGGAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGCTGAAAGAGCT 2050
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Qy  2111 CGCCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTCAGCTCACCCC 2170
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Qy  2171 GATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCTGGGCCGTGCA 2230
Db  2041 GATGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCTGGGCCGTGCA 2100
Qy  2231 AACCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACATTCAGATCCC 2290
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Qy  2291 CAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCGTGCAGGACTC 2350
Db  2161 CAAGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCGTGCAGGACTC 2220
Qy  2351 ACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCAT 2410
Db  2221 ACAGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCAT 2280
Qy  2411 GAGGCTCAAATCTCCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGT 2470
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Qy  2471 GGAACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGCACCTTGGGGT 2530
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Qy  3311 GGGGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGCCCAAGGTCTA 3370
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Qy  3431 GCCAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGGCCCACACCCT 3490
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Qy   3491 GAAGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGGACTATTTCTT 3550
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RESULT 15
HSU05810
LOCUS       HSU05810                3855 bp    mRNA    linear   PRI 07-DEC-1994
DEFINITION  Human inducible nitric oxide synthase mRNA, complete cds.
ACCESSION   U05810
VERSION     U05810.1  GI:452487
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3855)
  AUTHORS   Maier,R., Bilbe,G., Rediske,J. and Lotz,M.
  TITLE     Inducible nitric oxide synthase from human articular chondrocytes:
            cDNA cloning and analysis of mRNA expression
  JOURNAL   Biochim. Biophys. Acta 1208 (1), 145-150 (1994)
  MEDLINE   94368816
   PUBMED   7522054
REFERENCE   2  (bases 1 to 3855)
  AUTHORS   Maier,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JAN-1994) Rainer Maier, Medicine, University of
            California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0663,
            USA
FEATURES             Location/Qualifiers
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                     EHLARVEAVTKEIETTVTYQLTGDELIFATKQAWRNAPRCIGRIQWSNLQVFDARSCS
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     3'UTR           3657. .3855
BASE COUNT      894 a   1136 c   1067 g    758 t
ORIGIN

  Query Match           73.3%;  Score 3039;  DB 9;  Length 3855;
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Qy    193 GTAAAGCCATAGAGATGGCCTGTCCTTGGAAATTTCTGTTCAAGACCAAATTCCACCAGT 252
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Qy    793 ATGCCCCACGCTGCATTGGGAGGATCCAGTGGTCCAACCTGCAGGTCTTCGATGCCCGCA 852
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Qy    853 GCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCACCA 912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCTGTTCCACTGCCCGGGAAATGTTTGAACACATCTGCAGACACGTGCGTTACTCCACCA 900

Qy    913 ACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCACG 972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ACAATGGCAACATCAGGTCGGCCATCACCGTGTTCCCCCAGCGGAGTGATGGCAAGCACG 960
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Qy    973 ACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCA 1032
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCA 1020

Qy   1033 GCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCGACCTGGGCTGGA 1092
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGCTGTGCATCGACCTGGGCTGGA 1080

Qy   1093 AGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGACC 1152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGCCCAAGTACGGCCGCTTCGATGTGGTCCCCCTGGTCCTGCAGGCCAATGGCCGTGACC 1140

Qy   1153 CTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAAAT 1212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CTGAGCTCTTCGAAATCCCACCTGACCTTGTGCTTGAGGTGGCCATGGAACATCCCAAAT 1200

Qy   1213 ACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACATGC 1272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ACGAGTGGTTTCGGGAACTGGAGCTAAAGTGGTACGCCCTGCCTGCAGTGGCCAACATGC 1260

Qy   1273 TGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGGCA 1332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGCTTGAGGTGGGCGGCCTGGAGTTCCCAGGGTGCCCCTTCAATGGCTGGTACATGGGCA 1320

Qy   1333 CAGAGATCGGAGTCCGGGACTTCTGTGACGTCCAGCGCTACAACATCCTGGAGGAAGTGG 1392
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   1321 CAGAGATCGGAGTCCGGGACTTCTGTGATGTCCAGCGCTACAACATCCTGGAGGAAGTGG 1380

Qy   1393 GCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGTCG 1452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGGAGAATGGGCCTGGAAACGCACAAGCTGGCCTCGCTCTGGAAAGACCAGGCTGTCG 1440

Qy   1453 TTGAGATCAACATTGCTGTGATCCATAGTTTTCAGAAGCAGAATGTGACCATCATGGACC 1512
          |||||||||||||||||||| |||||||||| ||||||||||||||||||||||||||||
Db   1441 TTGAGATCAACATTGCTGTGCTCCATAGTTTCCAGAAGCAGAATGTGACCATCATGGACC 1500

Qy   1513 ACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGGGG 1572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 ACCACTCGGCTGCAGAATCCTTCATGAAGTACATGCAGAATGAATACCGGTCCCGTGGGG 1560

Qy   1573 GCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGTGT 1632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GCTGCCCGGCAGACTGGATTTGGCTGGTCCCTCCCATGTCTGGGAGCATCACCCCCGTGT 1620

Qy   1633 TTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGCCT 1692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TTCACCAGGAGATGCTGAACTACGTCCTGTCCCCTTTCTACTACTATCAGGTAGAGGCCT 1680

Qy   1693 GGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAGAGATTCCATTGA 1752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGAAAACCCATGTCTGGCAGGACGAGAAGCGGAGACCCAAGAGAAGAGAGATTCCATTGA 1740

Qy   1753 AAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGACAATGGCGTCCC 1812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AAGTCTTGGTCAAAGCTGTGCTCTTTGCCTGTATGCTGATGCGCAAGACAATGGCGTCCC 1800

Qy   1813 GAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGGCGCTGGCCTGGG 1872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GAGTCAGAGTCACCATCCTCTTTGCGACAGAGACAGGAAAATCAGAGGCGCTGGCCTGGG 1860

Qy   1873 ACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCATGGATAAGTACA 1932
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Db   1861 ACCTGGGGGCCTTATTCAGCTGTGCCTTCAACCCCAAGGTTGTCTGCATGGATAAGTACA 1920

Qy   1933 GGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTACGTTTGGCAATG 1992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GGCTGAGCTGCCTGGAGGAGGAACGGCTGCTGTTGGTGGTGACCAGTACGTTTGGCAATG 1980

Qy   1993 GAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGCTGAAAGAGCTCA 2052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GAGACTGCCCTGGCAATGGAGAGAAACTGAAGAAATCGCTCTTCATGCTGAAAGAGCTCA 2040

Qy   2053 ACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACCCTCGGTTCTGCG 2112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 ACAACAAATTCAGGTACGCTGTGTTTGGCCTCGGCTCCAGCATGTACCCTCGGTTCTGCG 2100

Qy   2113 CCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTCAGCTCACCCCGA 2172
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Db   2101 CCTTTGCTCATGACATTGATCAGAAGCTGTCCCACCTGGGGGCCTCTCAGCTCACCCCGA 2160

Qy   2173 TGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCTGGGCCGTGCAAA 2232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TGGGAGAAGGGGATGAGCTCAGTGGGCAGGAGGACGCCTTCCGCAGCTGGGCCGTGCAAA 2220

Qy   2233 CCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACATTCAGATCCCCA 2292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CCTTCAAGGCAGCCTGTGAGACGTTTGATGTCCGAGGCAAACAGCACATTCAGATCCCCA 2280

Qy   2293 AGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCGTGCAGGACTCAC 2352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AGCTCTACACCTCCAATGTGACCTGGGACCCGCACCACTACAGGCTCGTGCAGGACTCAC 2340

Qy   2353 AGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCATGA 2412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AGCCTTTGGACCTCAGCAAAGCCCTCAGCAGCATGCATGCCAAGAACGTGTTCACCATGA 2400

Qy   2413 GGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGTGG 2472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GGCTCAAATCTCGGCAGAATCTACAAAGTCCGACATCCAGCCGTGCCACCATCCTGGTGG 2460

Qy   2473 AACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGCACCTTGGGGTTT 2532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 AACTCTCCTGTGAGGATGGCCAAGGCCTGAACTACCTGCCGGGGGAGCACCTTGGGGTTT 2520

Qy   2533 GCCCAGGCAACCAGCCGGCCCTGGTCCAAGGCATCCTGGAGCGAGTGGTGGATGGCCCCA 2592
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Qy   2593 CACCCCACCAGACAGTGCGCCTGGAGGACCTGGATGAGAGTGGCAGCTACTGGGTCAGTG 2652
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Db   2581 CACCCCACCAGGCAGTGCGCCTGGAGGCCCTGGATGAGAGTGGCAGCTACTGGGTCAGTG 2640

Qy   2653 ACAAGAGGCTGCCCCCCTGCTCACTCAGCCAGGCCCTCACCTACTCCCCGGACATCACCA 2712
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Qy   2713 CACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAGAAGAGCCTGAGA 2772
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Db   2701 CACCCCCAACCCAGCTGCTGCTCCAAAAGCTGGCCCAGGTGGCCACAGAAGAGCCTGAGA 2760

Qy   2773 GACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGAAGTTCACCAACA 2832
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Db   2761 GACAGAGGCTGGAGGCCCTGTGCCAGCCCTCAGAGTACAGCAAGTGGAAGTTCACCAACA 2820

Qy   2833 GCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGTCTGCTGGCTTCC 2892
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GCCCCACATTCCTGGAGGTGCTAGAGGAGTTCCCGTCCCTGCGGGTGTCTGCTGGCTTCC 2880

Qy   2893 TGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCTCCTCCCGGGATC 2952
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   2881 TGCTTTCCCAGCTCCCCATTCTGAAGCCCAGGTTCTACTCCATCAGCTCCCCCCGGGATC 2940

Qy   2953 ACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACACCGGAGATGGCC 3012
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   2941 ACACGCCCACGGAGATCCACCTGACTGTGGCCGTGGTCACCTACCACACCCGAGATGGCC 3000

Qy   3013 AGGGTCCCCTGCACCACGGTGTCTGCAGCACATGGCTCAACAGCCTGAAGCCCCAAGACC 3072
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   3001 AGGGTCCCCTGCACCACGGCGTCTGCAGCACATGGCTCAACAGCCTGAAGCCCCAAGACC 3060

Qy   3073 CAGTGCCCTGCTTTGTGCGGAATGCCAGCGCCTTCCACCTCCCCGAGGATCCCTCCCATC 3132
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   3061 CAGTGCCCTGCTTTGTGCGGAATGCCAGCGGCTTCCACCTCCCCGAGGATCCCTCCCATC 3120

Qy   3133 CTTGCATCCTCATCGGGCCTGGCACAGGCATCGTGCCCTTCCGCAGTTTCTGGCAGCAAC 3192
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Db    3121 CTTGCATCCTCATCGGGCCTGGCACAGGCATCGCGCCCTTCCGCAGTTTCTGGCAGCAAC 3180

Qy    3193 GGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCTTGGTGTTTGGGT 3252
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Db    3181 GGCTCCATGACTCCCAGCACAAGGGAGTGCGGGGAGGCCGCATGACCTTGGTGTTTGGGT 3240

Qy    3253 GCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGATGGCCCAGAAGG 3312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3241 GCCGCCGCCCAGATGAGGACCACATCTACCAGGAGGAGATGCTGGAGATGGCCCAGAAGG 3300

Qy    3313 GGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGCCCAAGGTCTATG 3372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301 GGGTGCTGCATGCGGTGCACACAGCCTATTCCCGCCTGCCTGGCAAGCCCAAGGTCTATG 3360

Qy    3373 TTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGCTCCACAAGGAGC 3432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361 TTCAGGACATCCTGCGGCAGCAGCTGGCCAGCGAGGTGCTCCGTGTGCTCCACAAGGAGC 3420

Qy    3433 CAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGGCCCACACCCTGA 3492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3421 CAGGCCACCTCTATGTTTGCGGGGATGTGCGCATGGCCCGGGACGTGGCCCACACCCTGA 3480

Qy    3493 AGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGGACTATTTCTTTC 3552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3481 AGCAGCTGGTGGCTGCCAAGCTGAAATTGAATGAGGAGCAGGTCGAGGACTATTTCTTTC 3540

Qy    3553 AGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTCGGTGCTGTATTTCCTTACGAGG 3612
           |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    3541 AGCTCAAGAGCCAGAAGCGCTATCACGAAGATATCTTTGGTGCTGTATTTCCTTACGAGG 3600

Qy    3613 CGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAGCGCTCTGAGGGC 3672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 CGAAGAAGGACAGGGTGGCGGTGCAGCCCAGCAGCCTGGAGATGTCAGCGCTCTGAGGGC 3660

Qy    3673 CTACAGGAGGGGTTAAAGCTGCCGGCACAGAACTTAAGGATGGAGCCAGCTCTGCATTAT 3732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    3733 CTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTAT 3792
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Db    3721 CTGAGGTCACAGGGCCTGGGGAGATGGAGGAAAGTGATATCCCCCAGCCTCAAGTCTTAT 3780

Qy    3793 TTCCTCAACGTTGCTCCCCATCAAGCCCTTTACTTGACCTCCTAACAAGTAGCACCCTGG 3852
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Qy    3853 ATTGATCGGAGCCTC 3867
           |||||||||||||||
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Search completed: March 14, 2003, 13:16:08
Job time : 10506 secs